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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:05:35 ; Search time 17.5 Seconds
(Without alignments)
98.565 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77
Sequence: 1 WNFAGIEAASAI0G 15

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEM_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	77	100.0	20	10 US-09-813-333-60	Sequence 1, Appl
3	77	100.0	95	9 US-08-805-427A-1	Sequence 4, Appl
4	77	100.0	403	9 US-09-805-427A-4	Sequence 173, Appl
5	77	100.0	404	9 US-09-805-427A-3	Sequence 172, Appl
6	77	100.0	404	10 US-09-791-171-173	Sequence 61, Appl
7	77	100.0	404	10 US-09-791-171-172	Sequence 59, Appl
8	66	85.7	20	9 US-10-044-703-61	Sequence 59, Appl
9	66	85.7	20	10 US-09-813-333-61	Sequence 59, Appl
10	60	77.9	13	9 US-10-044-703-59	Sequence 59, Appl
11	60	77.9	13	10 US-09-813-333-59	Sequence 59, Appl
12	41	53.2	463	9 US-10-156-761-12653	Sequence 155, App
13	39	50.6	9	10 US-09-916-201-13	Sequence 155, App
14	39	50.6	221	9 US-10-054-988-155	Sequence 155, App
15	39	50.6	221	10 US-09-739-254-155	Sequence 155, App
16	39	50.6	221	10 US-09-304-615-155	Sequence 155, App
17	39	50.6	239	9 US-10-103-313-351	Sequence 351, App
18	38	49.4	37	10 US-09-864-761-39026	Sequence 39026, A
19	37	48.1	153	10 US-09-925-301-1367	Sequence 1367, Ap

20	37	48.1	360	9 US-10-024-828-9	Sequence 9, Appl
21	37	47.4	739	9 US-10-156-761-10111	Sequence 10111, A
22	36.5	47.4	516	9 US-10-156-761-13151	Sequence 13151, A
23	36	46.8	98	10 US-09-894-018-101	Sequence 101, App
24	36	46.8	140	9 US-09-341-894-2	Sequence 30, Appl
25	36	46.8	254	9 US-09-902-525-30	Sequence 105, App
26	36	46.8	308	10 US-09-894-018-105	Sequence 107, App
27	36	46.8	308	10 US-09-894-018-107	Sequence 1, Appl
28	36	46.8	376	9 US-10-224-567-1	Sequence 5082, Ap
29	35.5	46.1	679	10 US-09-815-242-5082	Sequence 262, App
30	35	45.5	90	9 US-09-989-920-262	Sequence 18, Appl
31	35	45.5	159	9 US-09-882-691-18	Sequence 865, App
32	35	45.5	165	9 US-09-925-299-865	Sequence 865, App
33	35	45.5	165	10 US-09-925-299-865	Sequence 2, Appl
34	35	45.5	222	9 US-09-867-159A-2	Sequence 2, Appl
35	35	45.5	296	9 US-10-128-714-3095	Sequence 320, App
36	35	45.5	296	9 US-10-128-714-8095	Sequence 2, Appl
37	35	45.5	320	9 US-09-877-160-2	Sequence 79, Appl
38	35	45.5	320	9 US-09-847-208-79	Sequence 73, Appl
39	35	45.5	321	9 US-09-847-208-73	Sequence 3900, Ap
40	35	45.5	331	9 US-09-738-626-3900	Sequence 290, App
41	35	45.5	373	9 US-09-934-435-290	Sequence 320, App
42	35	45.5	482	9 US-10-153-668-320	Sequence 432, App
43	35	45.5	486	9 US-10-153-668-432	Sequence 170, App
44	35	45.5	489	9 US-09-934-455-170	Sequence 3710, Ap
45	35	45.5	495	9 US-09-738-626-3710	

ALIGNMENTS

RESULT 1
US-10-044-703-60
; Sequence 60, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-60

Query Match 100.0%; Score 77; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAI0G 15
Db 2 WNFAGIEAASAI0G 16

RESULT 2
US-09-813-333-60
; Sequence 60, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81

;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 60
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-60

Query Match 100.0%; Score 77; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIOG 15
DB 2 WNFAGIEAASAIOG 16

RESULT 3
US-09-805-427A-1
; Sequence 1, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-805-427A-1

Query Match 100.0%; Score 77; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIOG 15
DB 6 WNFAGIEAASAIOG 20

RESULT 4
US-09-805-427A-4
; Sequence 4, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-805-427A-4

Query Match 100.0%; Score 77; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIOG 15
DB 27 WNFAGIEAASAIOG 41

RESULT 5

US-09-791-171-173
; Sequence 173, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Blak
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDRINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-173

Query Match 100.0%; Score 77; DB 10; Length 403;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIOG 15
DB 27 WNFAGIEAASAIOG 41

RESULT 6
US-09-805-427A-3
; Sequence 3, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-805-427A-3

Query Match 100.0%; Score 77; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIOG 15
DB 315 WNFAGIEAASAIOG 329

RESULT 7

US-09-791-171-172
; Sequence 172, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WEIDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: DERIVED FROM M. TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-172

Query Match 100.0%; Score 77; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NFAGIEAASAIQ 15
DB 315 NFAGIEAASAIQ 329

RESULT 8
US-10-044-703-61
; Sequence 61, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-61

Query Match 85.7%; Score 66; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NFAGIEAASAIQ 15
DB 1 NFAGIEAASAIQ 14

RESULT 9

US-09-813-333-61
; Sequence 61, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-61

Query Match 85.7%; Score 66; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NFAGIEAASAIQ 15
DB 1 NFAGIEAASAIQ 14

RESULT 10
US-10-044-703-59
; Sequence 59, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-59

Query Match 77.9%; Score 60; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NFAGIEAASAIQ 14
DB 1 NFAGIEAASAIQ 13

RESULT 11
US-09-813-333-59
; Sequence 59, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 59
; LENGTH: 13

;; TYPE: PRT
;; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-59

Query Match 77.9%; Score 60; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NFAGIEAASAIQ 14
DB 1 NFAGIEAASAIQ 13

RESULT 12
US-10-156-761-12653
; Sequence 12653, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12653
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12653

Query Match 53.2%; Score 41; DB 9; Length 463;
Best Local Similarity 53.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAI 13
DB 311 WNFAGIEAASAI 323

RESULT 13
US-09-916-201-13
; Sequence 13, Application US/09916201
; Patent No. US20020131976A1
; GENERAL INFORMATION:
; APPLICANT: LAIVANT, AJLE
; APPLICANT: PATHAN, ANSAR A.
; APPLICANT: HILL, ADRIAN V.S.
; TITLE OF INVENTION: TUBERCULOSIS VACCINE
; FILE REFERENCE: 117-359
; CURRENT APPLICATION NUMBER: US/09/916,201
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/467,893
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,783
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: M. tuberculosis
US-09-916-201-13

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Best Local Similarity 100.0%; Pred. No. 3.9e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GIEAASAI 13
DB 1 GIEAASAI 9

RESULT 14
US-10-054-988-155
; Sequence 155, Application US/10054988
; Publication No. US20030087341A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-054-988-155

Query Match 50.6%; Score 39; DB 9; Length 221;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
DB 132 WNFAGIEAASAIQ 145

RESULT 15
US-09-739-254-155
; Sequence 155, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 08/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PCT/US99/19330
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-254-155

Query Match 50.6%; Score 39; DB 10; Length 221;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Thu Jul 3 14:50:03 2003

us-09-830-839-6.rapb

Page 5

OY 1 MNFAGIEAASATQ 14
| | | | |
Db 132 MNLIGDEAAALAQ 145

Search completed: July 3, 2003, 14:08:27
Job time : 17.5 secs

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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:04:30 ; Search time 11 Seconds
(without alignments)
40.122 Million cell updates/sec

Title: US-09-830-839-6
Perfect score: 77
Sequence: 1 WNFAGIEAASAIQ 15

Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/aa/6B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	77	100.0	51	4	US-08-818-111-99
3	77	100.0	51	4	US-09-056-556-104
4	77	100.0	51	4	US-09-072-596-99
5	77	100.0	95	2	US-08-465-640-2
6	40	51.9	2293	4	US-09-368-590-2
7	38	49.4	418	4	US-09-202-893B-4
8	37	48.1	360	4	US-09-509-902A-9
9	35	45.5	29	2	US-08-482-142-11
10	35	45.5	29	2	US-08-482-142-74
11	35	45.5	29	2	US-08-478-572-11
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13	35	45.5	29	4	US-08-484-296-11
14	35	45.5	29	4	US-08-484-296-74
15	35	45.5	29	5	PCT-US95-04481-3
16	35	45.5	117	4	US-09-042-353-232
17	35	45.5	117	4	US-08-758-417A-80
18	35	45.5	159	4	US-09-347-803-18
19	35	45.5	222	1	US-07-945-288-11
20	35	45.5	222	1	US-08-462-831-11
21	35	45.5	222	1	US-08-461-809-11
22	35	45.5	222	1	US-08-461-441-11
23	35	45.5	222	1	PCT-US93-08518-11
24	35	45.5	245	1	US-07-945-288-2
25	35	45.5	245	1	US-08-462-831-2
26	35	45.5	245	1	US-08-461-809-2
27	35	45.5	245	1	US-08-461-441-2

28	35	45.5	245	2	US-08-482-142-2	Sequence 2, Appl1
29	35	45.5	245	2	US-08-478-572-2	Sequence 2, Appl1
30	35	45.5	245	3	US-08-460-040-2	Sequence 2, Appl1
31	35	45.5	245	4	US-08-484-296-2	Sequence 2, Appl1
32	35	45.5	245	5	PCT-US93-08518-2	Sequence 2, Appl1
33	35	45.5	320	1	US-07-945-288-10	Sequence 10, Appl1
34	35	45.5	320	1	US-08-462-831-10	Sequence 10, Appl1
35	35	45.5	320	1	US-08-461-809-10	Sequence 10, Appl1
36	35	45.5	320	1	US-08-482-142-6	Sequence 10, Appl1
37	35	45.5	320	1	PCT-US93-08518-10	Sequence 10, Appl1
38	35	45.5	321	1	US-07-945-288-6	Sequence 6, Appl1
39	35	45.5	321	1	US-08-462-831-6	Sequence 6, Appl1
40	35	45.5	321	1	US-08-461-809-6	Sequence 6, Appl1
41	35	45.5	321	1	US-08-461-441-6	Sequence 6, Appl1
42	35	45.5	321	2	US-08-482-142-6	Sequence 6, Appl1
43	35	45.5	321	2	US-08-478-572-6	Sequence 6, Appl1
44	35	45.5	321	4	US-08-484-296-6	Sequence 6, Appl1
45	35	45.5	321	5	PCT-US93-08518-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-818-112-104
Sequence 104, Application US/08818112

Patent No. 6290969

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvyck, Daniel S.
APPLICANT: Twartzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-818-112-104

Query Match 100.0% Score 77; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIQG 15
DB 6 WNFAGIEAASAIQG 20

RESULT 2

US-08-818-111-99
Sequence 99, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vardzik, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-99

Query Match 100.0%; Score 77; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIQG 15
DB 6 WNFAGIEAASAIQG 20

RESULT 3

US-09-056-556-104
Sequence 104, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle

TREATM

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-104

Query Match 100.0%; Score 77; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIQG 15
DB 6 WNFAGIEAASAIQG 20

RESULT 4

US-09-072-596-99
Sequence 99, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vardzik, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-99

Query Match 100.0%; Score 77; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQG 15
|||||
DB 6 WNFAGIEAASAIQG 20

RESULT 5

US-08-465-640-2
Sequence 2, Application US/08465640
Patent No. 5953077

GENERAL INFORMATION:

APPLICANT: ANDERSEN, Peter
APPLICANT: ANDERSEN, Ase Bengaard
APPLICANT: HASLOV, Kaare
APPLICANT: SORENSEN, Anne Lund
TITLE OF INVENTION: TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,640
FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,182
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK94/00273
FILING DATE: 01-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSEN-3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-640-2

Query Match 100.0%; Score 77; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQG 15
|||||

DB 6 WNFAGIEAASAIQG 20

RESULT 6

US-09-368-590-2
Sequence 2, Application US/09368590
Patent No. 6187563

GENERAL INFORMATION:

APPLICANT: Solimena, Michele
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2293
TYPE: PRT
ORGANISM: Human
US-09-368-590-2

Query Match 51.9%; Score 40; DB 4; Length 2293;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
|:|:|:|:|:
DB 720 WRLSGLEAALQALE 733

RESULT 7

US-09-202-893B-4
Sequence 4, Application US/09202893B
Patent No. 6319692

GENERAL INFORMATION:

APPLICANT: KADOTA, Mariko
APPLICANT: KIMAKI, Mayumi
APPLICANT: SAWAKI, Saeko
APPLICANT: SHIRASAWA, Yukiko
APPLICANT: SONE, Harue
APPLICANT: SAKO, Tomoyuki
TITLE OF INVENTION: METHODS FOR TRANSFERRING GENE INTO CHROMOSOME
FILE REFERENCE: 980794/HG
CURRENT APPLICATION NUMBER: US/09/202,893B
CURRENT FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: PCT/JP97/02187
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: JP 8/184266
PRIOR FILING DATE: 1996-06-26
PRIOR APPLICATION NUMBER: JP 8/257764
PRIOR FILING DATE: 1996-09-06
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 418
TYPE: PRT
ORGANISM: Lactobacillus casei
US-09-202-893B-4

Query Match 49.4%; Score 38; DB 4; Length 418;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 FAGIEAASAIQG 15
|||:|:|:|:
DB 31 FARIKAAAKKYQG 43

RESULT 8

US-09-509-902A-9
Sequence 9, Application US/09509902A

Patent No. 6387676
GENERAL INFORMATION:
APPLICANT: Virca, Duke
APPLICANT: Bird, Timothy A.
APPLICANT: Anderson, Dirk M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: Human CDNs Encoding Polypeptides Having Kinase Functions
FILE REFERENCE: 2877-US
CURRENT APPLICATION NUMBER: US/09/509,902A
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 9
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-509-902A-9

Query Match 48.1%; Score 37; DB 4; Length 360;
Best Local Similarity 50.0%; Pred. No. 78;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNFAGTEAASA 12
Db 4 WSWAGIPSSAA 15

RESULT 9

US-08-482-142-11
Sequence 11, Application US/08482142
Patent No. 5820862

GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLEGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017,605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-482-142-11

Query Match 45.5%; Score 35; DB 2; Length 29;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 WNFAGTEAASA 12
Db 15 WAFSGVAATESA 26

RESULT 10

US-08-482-142-74
Sequence 74, Application US/08482142
Patent No. 5820862

GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLEGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017,605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-482-142-74

Query Match 45.5%; Score 35; DB 2; Length 29;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 WNFAGTEAASA 12
Db 15 WAFSGVAATESA 26

```

1  APPLICANT: Shaked, Ze'ev
2  TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
3  TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
4  NUMBER OF SEQUENCES: 207
5  CORRESPONDENCE ADDRESSES:
6  ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
7  STREET: 610 LINCOLN STREET
8  CITY: WALTHAM
9  STATE: MA
10 COUNTRY: USA
11 ZIP: 02154
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17
18 SOFTWARE: ASCII TEXT
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/478,572
22 FILING DATE: 07-June-1995
23
24 CLASSIFICATION:
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/445,307
28 FILING DATE:
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: CRAIG, ANNE I.
32 REGISTRATION NUMBER: 32,976
33 REFERENCE/DOCKET NUMBER: 017.605
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (617) 466-6000
36 TELEFAX: (617) 466-6040
37
38 INFORMATION FOR SEQ ID NO: 74:
39
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 29 amino acids
42 TYPE: amino acid
43 TOPOLOGY: linear
44 MOLECULE TYPE: peptide
45 FRAGMENT TYPE: N-terminal
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47 US-08-478-572-74
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017,605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ. ID NO.: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-484-296-11

Query Match 45.5%; Score 35; DB 4; Length 29;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAASA 12
| | | | |
DB 15 WAFSGVAATESA 26

RESULT 14
US-08-484-296-74
Sequence 74, Application US/08484296
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mel-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976

REFERENCE/DOCKET NUMBER: 017,605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ. ID NO.: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-484-296-74

Query Match 45.5%; Score 35; DB 4; Length 29;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAASA 12
| | | | |
DB 15 WAFSGVAATESA 26

RESULT 15
PCT-US95-04481-3
Sequence 3, Application PC/TUS9504481
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dust M
NUMBER OF SEQUENCES: 54
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04481
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,772
FILING DATE: April 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 017.5 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ. ID NO.: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
PCT-US95-04481-3

Query Match 45.5%; Score 35; DB 5; Length 29;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAASA 12
| | | | |
DB 15 WAFSGVAATESA 26

Search completed: July 3, 2003, 14:07:46
Job time : 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2003, 14:03:09 ; Search time 24 Seconds
(without alignments)
128.779 Million cell updates/sec

Title: US-09-830-839-6
Perfect score: 77
Sequence: 1 MNFAGIEAASAIQG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	61.0	714	16	09CESS5
2	44	57.1	225	2	09RFF6
3	42.5	55.2	141	16	09HYR3
4	42	54.5	369	16	09ZB39
5	41	54.5	2030	10	08RZC9
6	42	53.2	440	2	09FAD1
7	41	53.2	443	2	09AMK7
8	41	53.2	445	16	09KV76
9	41	53.2	340	16	09CGX6
10	41	51.9	803	5	09N978
11	40	51.9	134	8	09XMD0
12	40	51.9	134	8	09XMD1
13	40	51.9	323	16	08UH81
14	40	51.9	330	17	027223
15	40	51.9	379	8	09B1N0
16	40	51.9	379	8	09B1O6

17	40	51.9	379	8	09B0Y1	09B0Y1 pteronotus
18	40	51.9	379	8	09B0U6	09B0U6 pteronotus
19	40	51.9	379	8	09B0S2	09B0S2 pteronotus
20	40	51.9	379	8	09B377	09B377 pteronotus
21	40	51.9	379	8	09B376	09B376 pteronotus
22	40	51.9	379	8	09B375	09B375 pteronotus
23	40	51.9	379	8	09B374	09B374 pteronotus
24	40	51.9	379	8	09B373	09B373 pteronotus
25	40	51.9	379	8	09B372	09B372 pteronotus
26	40	51.9	379	8	09B371	09B371 pteronotus
27	40	51.9	379	8	09B369	09B369 pteronotus
28	40	51.9	379	8	09B368	09B368 pteronotus
29	40	51.9	379	8	09B367	09B367 pteronotus
30	40	51.9	379	8	09B366	09B366 pteronotus
31	40	51.9	379	8	09B365	09B365 pteronotus
32	40	51.9	379	8	09B364	09B364 pteronotus
33	40	51.9	379	8	08WDK6	08WDK6 pteronotus
34	40	51.9	419	10	094LJ5	094LJ5 oryza sativ
35	40	51.9	493	16	092VB8	092VB8 rhizobium m
36	40	51.9	536	17	09HNR2	09HNR2 halobacteri
37	40	51.9	1005	12	09Q937	09Q937 shope fibro
38	40	51.9	1006	12	09Q8R2	09Q8R2 myxoma viru
39	40	51.9	2555	11	0912E6	0912E6 mus musculu
40	40	51.9	2561	11	08V1E5	08V1E5 mus musculu
41	39	50.6	101	17	0589J24	0589J24 pyrococcus
42	39	50.6	120	8	08WCZ5	08WCZ5 articocephal
43	39	50.6	120	8	08WCZ4	08WCZ4 articocephal
44	39	50.6	120	8	08WCZ3	08WCZ3 articocephal
45	39	50.6	120	8	08WCZ1	08WCZ1 eumetoplas

ALIGNMENTS

RESULT 1
ID 09CESS5 PRELIMINARY; PRT; 714 AA.
DC 09CESS5;
DT 01-JUN-2001 (TREMBLrel. 17, created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Glutamine ABC transporter permease and substrate binding protein
GN protein.
GN GMP OR LI1759.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacilli/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Boletini A., Wincker P., Manger S., Jallion O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
RT Genome Res. 11:731-753(2001).
RL
-1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
EMBL: AE006406; AK05857.1; -;
HSSP: P10344; IWDN.
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR001311; SBP/glu_receptor.
DR InterPro: IPR001638; SBP_bac_3.
DR Pfam: PF00528; BPD_transp.1.
DR Pfam: PF00497; SBP_bac_3; 2.
DR SMART: SM0062; PBD; 2.
DR PROSITE: PS00402; BPD_TRANS_PNN_MEMBR; 1.
DR PROSITE: PS01039; SBP_BACTERIAL_3; UNKNOWN_1.

KW Transmembrane; Transport; Complete proteome.
SQ SEQUENCE 714 AA; 78377 MW; 4EBB8E5453A968EB CRC64;

Query Match 61.0%; Score 47; DB 16; Length 714;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIQ 14
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Db 303 WNFAGIEAASAIQ 316

RESULT 2

O9RFF6 PRELIMINARY; PRT; 225 AA.
AC O9RFF6: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2002 (TREMBLrel. 20, Last annotation update)
DE Ured.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OX NCBI_TaxID=1063;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=2.4.1;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
RT sphaeroides 2.4.1.";
RL Nucleic Acids Res. 0:0-0(2000).
DR EMBL; AF195122; AAF24251.1; -;
DR InterPro: IPR002669; Ured.
DR Pfam: PF01774; Ured; 1.
SQ SEQUENCE 225 AA; 23417 MW; 59EC44A05802C29F CRC64;

Query Match 57.1%; Score 44; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 AGIEAASAIQ 15
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Db 178 AGIEAASAIQ 189

RESULT 3

O9HYR3 PRELIMINARY; PRT; 141 AA.
AC O9HYR3: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Hypothetical protein PA3332.
GN PA3332.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004755; AAC06720.1; -;
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 141 AA; 15920 MW; 9C0CF669C6C0C5BB CRC64;

Query Match 55.2%; Score 42.5; DB 16; Length 141;
Best Local Similarity 40.9%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

OY 1 WN-----FAGIEAASAIQ 15
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Db 119 WNPRLRLALGVEAASAIQ 140

RESULT 4

O9Z839 PRELIMINARY; PRT; 369 AA.
AC O9Z839: 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FE-S oxidoreductase.
GN CPN0513 OR CPJ0513 OR CP0240.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CML029;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olmiger L., Grimwood J., Davis R.W., Stephens R.S., Trachomatis.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Morn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kunara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AE001636; AAD18653.1; -;
DR EMBL; AE002184; AAF38105.1; -;
DR EMBL; AF002546; BAA98719.1; -;
DR TIGR; CP0240; -;
DR InterPro: IPR005244; Cons_hypoth423.
DR TIGR; TIGR00423; TIGR00423; 1.
KW Complete proteome.

SQ SEQUENCE 369 AA; 41556 MW; 05AC33C15479B192 CRC64;

Query Match 54.5%; Score 42; DB 16; Length 369;
Best Local Similarity 77.8%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNFAGIEA 9
||:|||||
Db 305 WNFAGIEA 313

RESULT 5

O8RZC9 PRELIMINARY; PRT; 2030 AA.
ID O8RZC9

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AC Q8R2C9;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE P0510C12.24 protein.
GN P0510C12.24
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0510C12."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AP003725; BAB90479.1;
SQ SEQUENCE 2030 AA; 223434 MW; 26C042AD2D4867ED CRC64;

Query Match 54.5%; Score 42; DB 10; Length 2030;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI0G 15
DB 400 WNSSGSCNAASAPG 414

RESULT 6
O9FAD1 PRELIMINARY; PRT; 440 AA.
ID O9FAD1
AC O9FAD1
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CADB.
GN CADB.
OS Moritella japonica.
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Moritella.
OX NCBI_TaxID=89067;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSK1;
RA Li L., Fujii S., Kato C., Koki H.;
RT "Expression of Lysin Decarboxylase Gene Is Regulated by Pressure in a
RT Deep-Sea Piezophilic Bacterium, Moritella japonica."
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB041735; BAB16717.1;
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
SQ SEQUENCE 440 AA; 45577 MW; DBDEACADRF8958CD9 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 440;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI 10
DB 199 WSFVGVESAA 208

RESULT 7
O9AMK7 PRELIMINARY; PRT; 443 AA.
ID O9AMK7
AC O9AMK7
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cadaverine/lysine antiporter.

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GN CADB.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhee J., Lee J., Lee S., Chung S., Rhee J., Choi S., Ryu P.;
RT "Vibrio vulnificus cdda genes."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF324470; AAK01663.1;
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
SQ SEQUENCE 443 AA; 46752 MW; B88FD7E18036751 CRC64;

Query Match 53.2%; Score 41; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI 10
DB 199 WSFVGVESAA 208

RESULT 8
O9KV76 PRELIMINARY; PRT; 445 AA.
ID O9KV76
AC O9KV76
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cadaverine/lysine antiporter Cadb, putative.
GN VC0280.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE-20406833; PubMed-10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Rettell H., Dragoi I., Sellers P.,
RA Ermlaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Uterback T., Fleischmann R.D., Niernan W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004116; AAF93455.1;
DR TIGR; VC0280;
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KV Complete proteome.
SQ SEQUENCE 445 AA; 46907 MW; 3A6F21B9680584C CRC64;

Query Match 53.2%; Score 41; DB 16; Length 445;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI 10
DB 199 WSFVGVESAA 208

RESULT 9
O9CGX6 PRELIMINARY; PRT; 540 AA.
ID O9CGX6
AC O9CGX6
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

```

DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE ABC transporter permease protein.
 GN YJ02 OR L10966.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria: Firmicutes: Bacillus/Clostridium group: Lactobacillales:
 OC Streptococcaceae: Lactococcus.
 NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IL1403;
 RX MEDLINE-21235186; PubMed-11337471;
 RA Bioclin A., Wincker P., Manger S., Jallion O., Malarne K.,
 RT Weissbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403."
 RL Genome Res. 11:731-753(2001).
 DR EMBL: AE006331; AAK05064.1; -.
 KM Complete proteome.
 SO SEQUENCE 540 AA; 60283 MW; E896CF783987560E CRC64;

Query Match 53.2%; Score 41; DB 16; Length 540;
 Best Local Similarity 69.2%; Pred. No. 1.4e+02;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FAGEAASAIQ 15
 DB 339 FVGNETAASAIRG 351

RESULT 10

Q9N978 PRELIMINARY; PRT; 803 AA.
 AC Q9N978;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Possible amino acid transporter.
 GN P1295.10.
 OS Leishmania major.
 OC Eukaryota: Euglenozoa: Kinetoplastida: Trypanosomatidae: Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,
 RA Andrejaski M.A., Barrell B.G.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RX MEDLINE-9816435; PubMed-9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome."
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL359773; CAB95218.1; -.
 DR InterPro: IPR002293; AA/rel_primease1.
 DR InterPro: IPR004841; Permease.
 DR Pfam: PF00324; aa_permeases; 1.
 SO SEQUENCE 803 AA; 84779 MW; 0AEBD76516440558 CRC64;

Query Match 53.2%; Score 41; DB 5; Length 803;
 Best Local Similarity 42.9%; Pred. No. 2.1e+02;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
 DB 285 WNFANIEAGAVE 298

RESULT 11

Q9XMD0 PRELIMINARY; PRT; 134 AA.
 ID Q9XMD0

AC Q9XMD0;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE Cytochrome b (Fragment).
 GN Cytb.
 OS Pteronotus davidi (Davy's naked-backed bat).
 OG Mitochondrion.
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi;
 OC Mammalia: Eutheria: Chiroptera: Microchiroptera: Mormoopidae;
 OC Pteronotus.
 NCBI_TaxID=94956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20072938; PubMed-10603267;
 RA Kennedy M., Paterson A.M., Morales J.C., Parsons S., Winington A.P.,
 RA Spencer H.G.;
 RT "The long and short of it: Branch lengths and the problem of placing
 RT the New Zealand short-tailed bat, Mystacina."
 RL Mol. Phylogenet. Evol. 13:405-416(1999).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B565) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL: AF144070; AAD34999.1; -.
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF00033; Cytochrome_b_N; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 KM Electron transport; Heme; Mitochondrion; Respiratory chain;
 KM Transmembrane.
 FT NON_TER 134 134
 SO SEQUENCE 134 AA; 15054 MW; 54FA6146B46D3C03 CRC64;

Query Match 51.9%; Score 40; DB 8; Length 134;
 Best Local Similarity 50.0%; Pred. No. 50;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAIQ 14
 DB 31 WNFGLAACLAVQ 44

RESULT 12

Q9XMD1 PRELIMINARY; PRT; 134 AA.
 AC Q9XMD1;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE Cytochrome b (Fragment).
 GN Cytb.
 OS Pteronotus parnellii (Parnell's mustached bat).
 OG Mitochondrion.
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi;
 OC Mammalia: Eutheria: Chiroptera: Microchiroptera: Mormoopidae;
 OC Pteronotus.
 NCBI_TaxID=59476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20072938; PubMed-10603267;
 RA Kennedy M., Paterson A.M., Morales J.C., Parsons S., Winington A.P.,
 RA Spencer H.G.;
 RT "The long and short of it: Branch lengths and the problem of placing
 RT the New Zealand short-tailed bat, Mystacina."
 RL Mol. Phylogenet. Evol. 13:405-416(1999).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

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CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL: AF144071; AAD35000.1; -.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF000033; cytochrome_b_n_1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON TER 134
SQ SEQUENCE 134 AA; 15086 MW; 5068D4E9AA6D23C4 CRC64;

Query Match 51.9%; Score 40; DB 8; Length 134;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 WNFAGIEAASAIQ 14
Db 31 WNFSGSLAACLAQ 44

RESULT 13
ID Q8UH81 PRELIMINARY; PRT; 323 AA.
AC Q8UH81;
DT 01-JUN-2002 (TRENBLREL 21, Created)
DT 01-JUN-2002 (TRENBLREL 21, Last sequence update)
DE 01-JUN-2002 (TRENBLREL 21, Last annotation update)
DE Hypothetical protein Atu0802.
GN Atu0802 OR AGR_C1468.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608550; PubMed-11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitaajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayian T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao H., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608551; PubMed-11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iatkenouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughly D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Clelo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009047; AAL41818.1; -.
DR EMBL: AE008013; AKK6611.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 323 AA; 35066 MW; C2097F09A00C744E CRC64;

Query Match 51.9%; Score 40; DB 16; Length 323;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Oy 3 FAGIEAASAIQ 15
Db 11 FAGISCAATALAG 23

RESULT 14
ID 027223 PRELIMINARY; PRT; 330 AA.
AC 027223;
DT 01-JAN-1998 (TRENBLREL 05, Created)
DT 01-JAN-1998 (TRENBLREL 05, Last sequence update)
DE 01-JUN-2002 (TRENBLREL 21, Last annotation update)
DE NA+/CA+ EXCHANGING protein related.
GN MTH1155.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-DELTA H;
RX MEDLINE-98037514; PubMed-9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert R.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadatoria R., Vlcare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mo J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000885; AAB85644.1; -.
DR InterPro: IPR004481; K_NacCaexchng.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR TIGRFAMs: TIGR00367; K_NacCaexchng-rel; 1.
KW Complete proteome.
SQ SEQUENCE 330 AA; 34762 MW; BEE7B029F5A54DF CRC64;

Query Match 51.9%; Score 40; DB 17; Length 330;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 1 WNFAGIEAASAIQ 15
Db 95 WNIAGILGISSVAG 109

RESULT 15
ID 09B1N0 PRELIMINARY; PRT; 379 AA.
AC 09B1N0;
DT 01-JUN-2001 (TRENBLREL 17, Created)
DT 01-JUN-2001 (TRENBLREL 17, Last sequence update)
DE 01-OCT-2001 (TRENBLREL 18, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Pteronotus davyi (Davy's naked-backed bat).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Mormoopidae;
OC Pteronotus.
OX NCBI_TaxID=94956;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-27642, AND 35483;
RA Lewis-Orlit N., Porter C.A., Baker R.J.;
RT "Molecular systematics of the Family Mormoopidae (Chiroptera) Based on
RT Mitochondrial cytochrome b and Nuclear RAG-2 Gene Sequences."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBQUITINOL-CYTOCHROME C REDUCTASE

```

CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL: AF338672; AAK21932.1; -
DR EMBL: AF338670; AAK21930.1; -
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF000033; cytochrome_b_c1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME_1.
DR PROSITE: PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SO SEQUENCE 379 AA; 42664 MW; 27FC6661E686E624 CRC64;

Query Match 51.98; Score 40; DB 8; Length 379;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WNFAGTEAASATQ 14
|||: || -1
Db 31 WNFGLAACLAAYQ 44

Search completed: July 3, 2003, 14:06:48
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:02:14 ; Search time 6.5 Seconds

(Without alignments)
95.715 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 MNFAGIEAASATIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	77	100.0	94	1	ESAB_MYCTU
2	43	55.8	476	1	NOEA_RHIME
3	41	53.2	384	1	PHUB_BACSU
4	40	51.9	294	1	G3P_ESCHL
5	40	51.9	2564	1	SPCO_HUMAN
6	39	50.6	370	1	CYB_EPRCE
7	39	50.6	379	1	CYB_ZALCA
8	39	50.6	425	1	PELD_ERWCH
9	39	50.6	445	1	YUDE_ECOLI
10	39	50.6	990	1	NSP7_ECOLI
11	38	49.4	95	1	ESAB_MYCLE
12	38	49.4	444	1	CADR_ECOLI
13	38	49.4	923	1	YAUD_SCHPO
14	38	49.4	962	1	ARVC_HUMAN
15	38	49.4	969	1	ARVC_MOUSE
16	38	49.4	988	1	TNP2_ECOLI
17	37	48.1	75	1	OCTL_MACEU
18	37	48.1	196	1	RBMS_XENLA
19	37	48.1	335	1	YD59_SCHPO
20	37	48.1	379	1	CYB_CHEMA
21	37	48.1	379	1	CYB_ZAPPR
22	37	48.1	404	1	DGIA_RHITO
23	37	48.1	475	1	GUWA_CLOCE
24	37	48.1	492	1	HUPR_RHOCA
25	37	48.1	507	1	PSBB_STNY3
26	37	48.1	509	1	PSBB_STNY3
27	37	48.1	509	1	PSBB_STNY3
28	37	48.1	660	1	PAB3_ARATP
29	36	46.8	145	1	CYCP_RHOCA
30	36	46.8	145	1	Y008_MYCTU
31	36	46.8	211	1	MT04_STNY3
32	36	46.8	376	1	FDH_ORISA
33	36	46.8	377	1	FDH_HORVU

ALIGNMENTS

RESULT 1	ID	ESAB_MYCTU	STANDARD	PRT	94 AA.
AC	057165	084901			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	6 kDa early secretory antigenic target (ESAT-6).				
GN	ESAT6 OR RV3875 OR MT3989 OR MTW027.10.				
OS	Mycobacterium tuberculosis, and				
OS	Mycobacterium bovis.				
OC	Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;				
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OX	NCBI_Taxid=1773, 1765;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=M.tuberculosis; STRAIN=H37RV;				
RX	MEDLINE=95204931; PubMed=7897219;				
RA	Andersen P., Andersen A.B., Sorensen A.L., Nagai S.;				
RT	"Recall of long-lived immunity to Mycobacterium tuberculosis infection in mice.";				
RL	J. Immunol. 154:3359-3372(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=M.tuberculosis; STRAIN=H37RV;				
RX	MEDLINE=98295987; PubMed=9634230;				
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,				
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,				
RA	Badcock R., Basham D., Brown D., Chillingworth T., Connor R.,				
RA	Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,				
RA	Hornsby T., Jagels K., Krogh A., McLean A., Moule S., Murphy L.,				
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,				
RA	Ruster J.E., Taylor K., Skelton S., Squares R.,				
RA	Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;				
RT	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";				
RL	Nature 393:537-544(1998).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;				
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,				
RA	Peterson J.F., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,				
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,				
RA	Bisbal W., Uitterlind T., Weidman J., Khouri H., Gill J., Mikula A.,				
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";				
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				

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RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis;
RA Singh B., Siddiqui Z., Singh S., Sharma P.;
RT "ESAT-6 gene of a clinical isolate of Mycobacterium tuberculosis from
  India."
  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis;
RA Mahdires G.G., Sabo P.J., Hickey M.J., Singh D.C., Stover C.K.;
RT "Molecular analysis of genetic differences between Mycobacterium bovis
  BCG and virulent M. bovis."
  J. Bacteriol. 178:1274-1282(1996).
RN [7]
RP SEQUENCE OF 1-70 FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RA MEDLINE=99061212; PubMed=9846755;
RA Berthet F.X., Rasmussen P.B., Rosenkrands I., Andersen P.,
  Gicquel B.;
RT "A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel
  low-molecular-mass culture filtrate protein (CFP-10)."
  Microbiology 144:3195-3203(1998).
CC -1- FUNCTION: NOT KNOWN. ELICITS HIGH LEVEL OF INF-GAMMA FROM MEMORY
  EFFECTOR CELLS DURING THE FIRST PHASE OF A PROTECTIVE IMMUNE
  RESPONSE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U34848; AAC44033.1; -
DR EMBL: X79562; CAA56099.1; -
DR EMBL: AL022120; CAA17967.1; -
DR EMBL: AF420491; AAL16896.1; -
DR EMBL: AE007190; AAK48357.1; -
DR EMBL: AF004671; AAC83446.1; -
DR TIGR: MT3989; -
DR TubercuList: RV3875; -
KW Antigen: Complete.proteome.
FT INIT_MET 0
SQ SEQUENCE 94 AA; 9773 MW; 19245B0EC478BC84 CRC64;

Query Match 100.0%; Score 77; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 WNFAGIEAASAIQG 15
Db 5 WNFAGIEAASAIQG 19

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RX MEDLINE=96111489; PubMed=8801423;
RA Ardourel M., Lortet G., Maillet F., Roche P., Truchet G.,
  Prome J.-C., Rosenberg C.;
RT "In Rhizobium meliloti, the operon associated with the nod box n5
  comprises nodJ, noeA and noeB, three host-range genes specifically
  required for the nodulation of particular Medicago species."
  Mol. Microbiol. 17:687-699(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
  Barloy-Hubler F., Bowser L., Capela D., Gilbert F., Gouzy J.,
  Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
  Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
  Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
  Sinorhizobium meliloti pSymA megaplasmid."
  Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC -1- FUNCTION: NOT KNOWN. DOES NOT SEEM TO PARTICIPATE IN NOD FACTOR
  SYNTHESIS BUT REQUIRED FOR NODULATION ON SOME SPECIFIC MEDICAGO
  SPECIES SUCH AS M.LITTORALIS.
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U26430; AAC44091.1; -
DR EMBL: AE007232; AAK65074.1; -
DR InterPro: IPR000051; SAM_bind.
KW Plasmid; Nodulation; Complete proteome.
SQ SEQUENCE 476 AA; 53673 MW; EF0A4009B5F4965E CRC64;

Query Match 55.8%; Score 43; DB 1; Length 476;
Best Local Similarity 70.0%; Pred. No. 9.6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 WNFAGIEAANA 10
Db 101 WNFAGIEAANA 110

RESULT 3
FHUB_BACSU
ID FHUB_BACSU STANDARD; PRT; 384 AA.
AC P49936;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ferrichrome transport system permease protein fhub.
GN FHUB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Schneider R., Hantke K.;
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98304083; PubMed=9639930;
RA Wipat A., Brignell C.S., Guy J.B., Rose M., Emerson P.T.,
  Harwood C.R.;
RT "The ysa-yvga (293 degrees - 289 degrees) region of the Bacillus

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RT subtilis chromosome containing genes involved in metal ion uptake and
 RT a putative sigma factor.";
 RL Microbiology 144:1593-1600(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE-9804033; PubMed-9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boutsier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codan J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Meliade R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogilwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi V., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassaroiti A.,
 RA Viari A., Wambut R., Wedler H., Wedler H., Weltzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 RN [4]
 RP SEQUENCE OF 1-38 FROM N.A.
 RC STRAIN-168 / Marburg;
 RX MEDLINE-93268086; PubMed-838528;
 RA Schneider R., Hantke K.;
 RT "Iron-hydroxamate uptake systems in Bacillus subtilis: identification
 RT of a lipoprotein as part of a binding protein-dependent transport
 RT system.";
 RL Mol. Microbiol. 8:111-121(1993).
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED IN THE HIGH-
 CC AFFINITY TRANSPORT OF IRON(III)-FERRICHYDROXY INTO THE CELL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM PERMEASE FAMILY. PECCD SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X93092; CAA63643.1; -;
 DR EMBL: AJ223978; CAA11720.1; -;
 DR EMBL: 299121; CAB15337.1; -;
 DR EMBL: M87283; -; NOT_ANNOTATED_CDS.
 DR Subtilisin; Bg11389; fnub.
 DR InterPro: IPR000515; BPD_TRANSP.
 DR InterPro: IPR000522; PECCD.
 DR Pfam: PF01032; PECCD; 1.
 DR ProDom: PD001557; PECCD; 1.
 DR PROSITE: PS00402; BPD_TRANSP_INN_MEMBER; FALSE_NEG.
 DR Transprot: Iron transport; Transmembrane; Complete proteome.
 KW TRANSMEM 58 78 POTENTIAL.

FT TRANSMEM 115 135 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 176 196 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 243 263 POTENTIAL.
 FT TRANSMEM 296 316 POTENTIAL.
 FT TRANSMEM 330 350 POTENTIAL.
 FT TRANSMEM 357 377 POTENTIAL.
 SQ SEQUENCE 384 AA; 40720 MW; 7E4D75CAB36AB8FB CRC64;
 Query Match 53.2%; Score 41; DB 1; Length 384;
 Best Local Similarity 46.7%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 WNFAGIEAASAIQ 15
 DB 174 WSFAGAGASTVMG 188
 RESULT 4
 G3P_ESCBL STANDARD: PRT: 294 AA.
 ID G3P_ESCBL
 AC P24749;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
 DE (Eragrostis).
 GN GAP.
 OS Escherichia blatae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=563;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29907, ATCC 33429, and ATCC 33430;
 RX MEDLINE-92065252; PubMed-1955870;
 RA Lawrence J.G., Ochman H., Harcl D.L.;
 RT "Molecular and evolutionary relationships among enteric bacteria.";
 RL J. Gen. Microbiol. 137:1911-1921(1991).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 CC DEHYDROGENASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M63358; AAA23837.1; -;
 DR EMBL: M63359; AAA23852.1; -;
 DR EMBL: M63360; AAA23855.1; -;
 DR HSP; P06977; IGAD.
 DR InterPro: IPR000173; GAP_dhdrogenase.
 DR Pfam: PF00044; gpdh; 1.
 DR Pfam: PF02800; gpdh.C; 1.
 DR PROSITE: PS00071; GAPDH; 1.
 KW Glycolysis; Oxidoreductase; NAD.
 KW NON_TER 1
 FT BINDING 135 135 GLYCERALDEHYDE 3-PHOSPHATE.
 FT ACT_SITE 162 162 ACTIVATES THIOL GROUP DURING CATALYSIS.
 FT NON_TER 294 294
 SQ SEQUENCE 294 AA; 31372 MW; 16562CB38177D8B CRC64;
 Query Match 51.9%; Score 40; DB 1; Length 294;
 Best Local Similarity 58.3%; Pred. No. 19;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MNFAGIEAASA 12
| | | | |
Db 70 MNFAGIEVVA 81

RESULT 5
SPCO_HUMAN STANDARD; PRT: 2564 AA.
ID SPCO_HUMAN Q9H254; Q9H368; Q9H1K7; Q9H1K8; Q9H1K9;
AC Q9H254; Q9H368; Q9H1K7; Q9H1K8; Q9H1K9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain 3)
DE (Beta-IV spectrin).
GN SPTBN4 OR SPTBN3 OR KRAA1642.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21316449; PubMed=11294830;
RA Tse M.T., Tang J., Jin O., Korsgren C., John K.M., Kung A.L.,
RA Gwynn B., Peters L.L., Lux S.E.;
RT "A new spectrin, beta-IV, has a major truncated isoform that
RT associates with promyelocytic leukemia protein nuclear bodies and the
RT nuclear matrix".
RL J. Biol. Chem. 276:23974-23985(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 TO 4).
RX MEDLINE=20539976; PubMed=11086001;
RA Bergs S., Aguijaro D., Dirix R.J., Maksimova E., Stabach P.,
RA Hermet J.-M., Zhang J.-P., Philbrick W., Slepnev V., Ort T.,
RA Solimena M.;
RT "BetaIV spectrin, a new spectrin localized at axon initial segments
RT and nodes of ranvier in the central and peripheral nervous system".
RL J. Cell Biol. 151:985-1002(2000).
RN [3]
RP SEQUENCE OF 386-2382 FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RA MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro".
RL DNA Res. 7:273-281(2000).
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic
CC islets.
CC -1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.
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CC -----
DR EMBL: AF311855; AAG42473.1; -
DR EMBL: AF082075; AAG38874.1; -
DR EMBL: AF004226; AAF93171.1; -
DR EMBL: AY004226; AAF93172.1; -
DR EMBL: AY004227; AAF93173.1; -
DR EMBL: AB046862; BAB13468.1; -
DR HSSP: 001082; 1BKR.
DR Gene: HGNC:14896; SPTBN4.

DR MIM: 606214; -
DR InterPro: IPR001589; Actbind_actin.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR001849; PH.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR001605; Spectrin_PH.
DR Pfam: PF00307; CH; 2.
DR Pfam: PF00435; spectrin; 56.
DR PRINTS: PR00683; SPECTRINPH.
DR SMART: SM00233; CH; 2.
DR SMART: SM00233; PH; 1.
DR SMART: SM00150; SPEC; 16.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PS00020; ACTININ_2; 1.
DR PROSITE: PS50021; CH; 2.
DR PROSITE: PS50003; PH_DOMAIN; 1.
KW Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
KW Alternative splicing.
FT DOMAIN 1 282
FT 1 165
FT DOMAIN 180 282
FT REPEAT 309 354
FT REPEAT 398 419
FT REPEAT 429 533
FT REPEAT 535 642
FT REPEAT 644 771
FT REPEAT 773 879
FT REPEAT 881 985
FT REPEAT 1019 1086
FT REPEAT 1088 1197
FT REPEAT 1199 1303
FT REPEAT 1305 1408
FT REPEAT 1410 1513
FT REPEAT 1515 1619
FT REPEAT 1621 1725
FT REPEAT 1727 1832
FT REPEAT 1834 1940
FT REPEAT 1942 2046
FT REPEAT 2048 2107
FT DOMAIN 2418 2527
FT VARSPLIC 1 1257
FT VARSPLIC 1258 1286
FT VARSPLIC 1287 1309
FT VARSPLIC 1310 2564
FT VARSPLIC 2113 2154
FT VARSPLIC 2155 2564
FT CONFLICT 604 608
FT CONFLICT 714 714
FT CONFLICT 1189 1189
FT CONFLICT 1193 1193
FT CONFLICT 1331 1331
SQ SEQUENCE 2564 AA; 288982 MW; 52CDE7D1D601ECC CRC64;
Query Match 51.9%; Score 40; DB 1; Length 2564;
Best local Similarity 42.9%; Pred. No. 14e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 MNFAGIEAASA 14
| | | | |
Db 1022 WRLSGLEALQALE 1035

RESULT 6
CYB_EPICE STANDARD; PRT: 370 AA.
ID CYB_EPICE Q48043;
AC Q48043;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome B.
 GN MTCYB OR COB OR CYTB.
 OS Epilochares cenchria.
 OC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Henophidia; Boidae;
 CC Boidae; Epicrates.
 OX NCBI_TaxID=51743;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Campbell B.N.;
 RT "Hic Surt Serpentes - molecular phylogenetics and the Boidae
 (Serpentes: Boidae).";
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 CC -----
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 CC -----
 DR EMBL: U69777; AAC01811.1; -;
 DR EMBL: U69778; AAC01812.1; -;
 DR InterPro: IPR000179; CYL_b_b6.
 DR Pfam: PF000032; cytochrome_b_c1.
 DR Pfam: PF000033; cytochrome_b_n; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_Q0; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; FALSE_NEG.
 KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 HM Heme.
 FT METAL 75 75 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 89 89 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 174 174 IRON 2 (HEME B562 AXIAL LIGAND).
 FT METAL 188 188 IRON 1 (HEME B566 AXIAL LIGAND).
 SQ SEQUENCE 370 AA; 41744 MW; A42257B25EDDE2B CRC64;
 Query Match 50.6%; Score 39; DB 1; Length 370;
 Best Local Similarity 50.0%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 1 WNFACIEAASAIQ 14
 DB 23 WNFSGMLACSLAQ 36
 RESULT 7
 CYB_ZALCA STANDARD; PRT; 379 AA.
 AC Q36266;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome B
 GN MTCYB OR COB OR CYTB.
 OS Zalophus californianus (California sealion).
 OC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Plinipedia; Otariidae; Zalophus.
 OX NCBI_TaxID=9704;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=95230701; PubMed=7714914;
 RA Arason U., Podin K., Gulberg A., Ledje C., Mouchaty S.;
 RT "A molecular view of pliniped relationships with particular emphasis
 on the true seals.";
 RL J. Mol. Evol. 40:78-85(1995).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS.
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 CC -----
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 CC -----
 DR EMBL: X82310; CAA57753.1; -;
 DR HSP; P00157; 1BE3.
 DR InterPro: IPR000179; CYL_b_b6.
 DR Pfam: PF000032; cytochrome_b_c1.
 DR Pfam: PF000033; cytochrome_b_n; 1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE: PS00193; CYTOCHROME_B_Q0; 1.
 KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 HM Heme.
 FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 182 182 IRON 2 (HEME B562 AXIAL LIGAND).
 FT METAL 196 196 IRON 1 (HEME B566 AXIAL LIGAND).
 SQ SEQUENCE 379 AA; 42520 MW; F74CD03BA27C24D4 CRC64;
 Query Match 50.6%; Score 39; DB 1; Length 379;
 Best Local Similarity 50.0%; Pred. No. 36;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 1 WNFACIEAASAIQ 14
 DB 31 WNFSGMLACSLAQ 44
 RESULT 8
 PELL_ERWCH STANDARD; PRT; 425 AA.
 ID PELL_ERWCH
 AC Q47473; O59421;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Pectate lyase I precursor (EC 4.2.2.2) (Pectate transeliminase).
 GN PELL.
 OS Erwinia chrysanthemi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EC16;
 RX MEDLINE=95362691; PubMed=7635842;
 RA Alfano J.R., Ham J.H., Collmer A.;
 RT "Use of Ynfact to clone a pel gene encoding a highly alkaline,
 RT asparagine-rich pectate lyase isozyme from an Erwinia chrysanthemi
 RT EC16 mutant with deletions affecting the major pectate lyase
 RT isozymes.";
 RL J. Bacteriol. 177:4553-4556(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3937;

RX MEDLINE-96020649; PubMed-8577252;
 RA Lojowska E., Masclaux C., Boccarda M., Robert-Baudouy J.,
 RA Hugouviex-Cotte-Patrat N.;
 RT "Characterization of the *pel* gene encoding a novel pectate lyase of
 RT *Chrysiobacterium* 3937".
 RL Mol. Microbiol. 16:1183-1195(1995).
 CC
 CC -1- FUNCTION: PRESENTS AN ENDO-CLEAVING ACTIVITY ON POLYGALACTURONATE
 CC OR PARTIALLY METHYLATED PECTIN.
 CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
 CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
 CC their non-reducing ends.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC INDUCTION: BY PECTIC CATABOLIC PRODUCTS AND AFFECTED BY GROWTH
 CC PHASE, TEMPERATURE, IRON STARVATION, OSMOLARITY, ANAEROBIOSIS,
 CC NITROGEN STARVATION AND CATABOLITE REPRESSION.
 CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 9.
 CC
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 CC
 CC EMBL: I42248; AAA99476.1; -;
 DR EMBL: X81136; CAA57041.1; -;
 KM Lyase; Signal; Calcium.
 FT STGNAL 1 25
 FT CHAIN 26 425
 FT VARIANT 49 425
 FT VARIANT 55 55
 FT VARIANT 59 59
 FT VARIANT 64 64
 FT VARIANT 70 70
 FT VARIANT 103 105
 FT VARIANT 147 147
 FT VARIANT 160 160
 FT VARIANT 219 219
 FT VARIANT 224 224
 FT VARIANT 261 261
 FT VARIANT 264 264
 FT VARIANT 328 328
 FT VARIANT 343 348
 FT VARIANT 362 362
 FT VARIANT 378 378
 FT VARIANT 390 390
 FT VARIANT 396 396
 FT VARIANT 425 425
 SQ SEQUENCE 425 AA; 45537 MW; BE2557332CF91F7 CRC64;
 Query Match 50.6%; Score 39; DB 1; Length 425;
 Best Local Similarity 46.7%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-95334362; PubMed-7610040;
 RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 RA Blattner F.R.;
 RT "Analysis of the *Escherichia coli* genome VI: DNA sequence of the
 RT region from 92.8 through 100 minutes".
 RL Nucleic Acids Res. 23:2105-2119(1995).
 RN [2]
 RP REVISIONS.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-9742617; PubMed-9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12".
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE-21074935; PubMed-11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postel G.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., DiMantola E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7".
 RL Nature 409:529-533(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / RIMD 0509952;
 RX MEDLINE-21156231; PubMed-11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shida T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12".
 RL DNA Res. 8:11-22(2001).
 CC
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Potential).
 CC -1- SIMILARITY: BELONGS TO THE ARCD/CAD/GERAB/LYSI FAMILY OF
 CC PERMEASES.
 CC
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 CC
 CC EMBL: U14003; AAA97015.1; ALT_FRAME.
 DR EMBL: U14003; AAA97014.1; ALT_FRAME.
 DR EMBL: AE000484; AAC7076.1; -;
 DR EMBL: AE005644; AAC59314.1; -;
 DR EMBL: AP002568; BAB38520.1; -;
 DR ECGene; EG12462; yjdB.
 DR InterPro; IPR002293; Aa/re1_pmease1.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF00324; aa_permeases; 1.
 KM Hypothetical protein; Transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 10 30
 FT TRANSMEM 39 59
 FT TRANSMEM 99 119
 FT TRANSMEM 123 143
 FT TRANSMEM 153 173
 FT TRANSMEM 197 217
 FT POTENTIAL.

FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 276 296 POTENTIAL.
 FT TRANSMEM 322 342 POTENTIAL.
 FT TRANSMEM 356 376 POTENTIAL.
 FT TRANSMEM 386 406 POTENTIAL.
 FT TRANSMEM 409 429 POTENTIAL.
 SQ SEQUENCE 445 AA; 46842 MW; 359F70C489A20663 CRC64;

Query Match 50.6%; Score 39; DB 1; Length 445;
 Best Local Similarity 50.0%; Pred. No. 42;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNFAGIEAASA 12
 Db 202 MSFIEGASASVA 213

RESULT 10
 ID TNP7_ECOLI STANDARD; PRT; 990 AA.
 AC P13694;
 DT 01-JUN-1990 (Rel. 13, Created)
 DT 01-JUN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transposase for transposon Tn3926.
 GN TNP4.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=89160328; PubMed=2537961;
 RA Turner A.K., Grinstead J.;
 RT "DNA sequence of the transposase gene of the class II transposon, Tn3926";
 RL Nucleic Acids Res. 17:1757-1757(1989).
 CC -1- FUNCTION: REQUIRED FOR TRANSPOSITION OF TRANSPOSON Tn3926.
 CC -1- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 7.
 CC -----
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 CC -----
 DR EMBL: X14236; CAA32453.1; -
 DR PIR: S03285; TOEC26.
 DR InterPro: IPR002513; Transposase_7.
 DR Pfam: PF01526; Transposase_7; 1.
 KW Transposable element; transposition; DNA-binding; DNA recombination.
 SQ SEQUENCE 990 AA; 111073 MW; 0664D1EFED038F606 CRC64;

Query Match 50.6%; Score 39; DB 1; Length 990;
 Best Local Similarity 46.7%; Pred. No. 86;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 MNFAGIEAASA 15
 Db 927 MNTVLERATSLARG 941

RESULT 11
 ID ESA6_MYCLE STANDARD; PRT; 95 AA.
 AC 050206; O33083;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 6 kda early secretory antigenic target homolog (ESAT-6-like protein)

DE (L-ESAT).
 GN ESAT6 OR ESX OR I45 OR ML0049 OR MLCB628.12C.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Wields B., Notenhoom T., Naafs B., Offringa R., Ottenhoff T.;
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eigemeier K., Parthill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garner T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moulé S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Bartell B.G.;
 RT "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.

CC -----
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 CC -----

DR EMBL: X90946; CAA62441.1; -
 DR EMBL: Y14967; CAA75200.1; -
 DR EMBL: AL583917; CAC29557.1; -
 DR Leproma; ML0049; -
 KW Complete proteome.
 FT CONFLICT 55 R -> Q (IN REF. 1).
 FT CONFLICT 90 M -> T (IN REF. 1).
 SQ SEQUENCE 95 AA; 10465 MW; B1526F78CB2AB8A1 CRC64;

Query Match 49.4%; Score 38; DB 1; Length 95;
 Best Local Similarity 33.3%; Pred. No. 15;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 MNFAGIEAASA 15
 Db 5 WHFPALGAVNELQG 19

RESULT 12
 ID CADB_ECOLI STANDARD; PRT; 444 AA.
 AC P23891;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable cadaverine/lysine antiporter.
 GN CADB OR B4132 OR Z5735 OR ECS5114.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92105022; PubMed=1370290;
 RA Watson N., Dunyak D.S., Rosey E.L., Slonczewski J.L., Olson E.R.;
 RT "Identification of elements involved in transcriptional regulation of

the Escherichia coli cad operon by external pH.";
 J. Bacteriol. 174:530-540(1992).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE-92210511; PubMed-1556085;
 Meng S.-Y., Bennett G.N.;
 "Nucleotide sequence of the Escherichia coli cad operon: a system for
 neutralization of low extracellular pH.";
 J. Bacteriol. 174:2659-2669(1992).
 [3]
 SEQUENCE FROM N.A.
 STRAIN-K12 / MG1655;
 MEDLINE-95334362; PubMed-7610040;
 Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 Blattner F.R.;
 "Analysis of the Escherichia coli genome VI: DNA sequence of the
 region from 92.8 through 100 minutes.";
 Nucleic Acids Res. 23:2105-2119(1995).
 [4]
 SEQUENCE FROM N.A.
 STRAIN-0157:H7 / EDL933 / ATCC 700927;
 MEDLINE-21074935; PubMed-11206551;
 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
 Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 Welch R.A., Blattner F.R.;
 "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";
 Nature 409:529-533(2001).
 [5]
 SEQUENCE FROM N.A.
 STRAIN-0157:H7 / RIMD 0509952;
 MEDLINE-21156231; PubMed-11258796;
 Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 Ikeda T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
 Kuhnra S., Shiba T., Hattori M., Shingawa H.;
 "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 DNA Res. 8:11-22(2001).
 [6]
 FUNCTION: PROBABLE CADUTERINE/LYSINE ANTIporter OR PART OF IT.
 [7]
 INDUCTION: AT LOW PH IN THE PRESENCE OF LYSINE AND ACETIVES
 MAXIMAL LEVEL UNDER ANAEROBIC CONDITIONS.
 [8]
 SIMILARITY: BELONGS TO THE ABCD/CADB/GERAB/LYSI FAMILY OF
 PERMEASES.

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 EMBL: M67452; AAA23532.1; -
 EMBL: M76411; AAA23535.1; -
 EMBL: U14003; AAA97032.1; -
 EMBL: AE000486; AAC77093.1; -
 EMBL: AE005647; AAG58332.1; -
 EMBL: AP002568; BAB38537.1; -
 PIR: B41968; B41968.
 PIR: A41848; A41842.
 Ecogene: EG10132; cadB.
 InterPro: IPR002293; AA/rel_pmeasel.
 InterPro: IPR004841; Permease.
 InterPro: IPR004754; R/O_antiport.
 Pfam: PF00324; aa-permeases.1.
 TIGRFAMs: TIGR00905; 2A0302.1.
 Transport: Antiport; Amino-acid transport; Transmembrane;
 Inner membrane; Complete proteome.
 TRANSMEM 7 27 POTENTIAL.

FT	TRANSMEM	35	55	POTENTIAL.
FT	TRANSMEM	68	88	POTENTIAL.
FT	TRANSMEM	95	115	POTENTIAL.
FT	TRANSMEM	123	143	POTENTIAL.
FT	TRANSMEM	149	169	POTENTIAL.
FT	TRANSMEM	193	213	POTENTIAL.
FT	TRANSMEM	222	242	POTENTIAL.
FT	TRANSMEM	250	270	POTENTIAL.
FT	TRANSMEM	273	293	POTENTIAL.
FT	TRANSMEM	323	343	POTENTIAL.
FT	TRANSMEM	354	374	POTENTIAL.
FT	TRANSMEM	384	404	POTENTIAL.
FT	TRANSMEM	405	425	POTENTIAL.
SO	SEQUENCE	444 AA;	46665 MW;	E87913B449B0500A CRC64;

Query Match
 Best Local Similarity 49.4%; Score 38; DB 1; Length 444;
 Matches 6; Conservative 60.0%; Pred. No. 61;
 2; Mismatches 2; Indels 0; Gaps 0;

OY	1	WNAFAGIEAAA	10
Db	198	WAFVGESEA	207

RESULT 13
 YAVA_SCHPO STANDARD; PRT; 923 AA.
 AC 01-0CT-1996 (rel. 34, Created)
 DT 01-0CT-1996 (rel. 34, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Hypothetical protein C26A3.10 in chromosome I.
 GN SPAC26A3.10.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RC MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkhardt G., Aert R., Robben J., Gymnopoulos B.,
 RA Wellens J., Vansteirels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer C., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Coffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garçon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 "The genome sequence of Schizosaccharomyces pombe.";
 Nature 415:871-880(2002).
 [1]
 FUNCTION: GTPase-activating protein for the ADP ribosylation
 factor family (potential).
 [2]
 SIMILARITY: CONTRAINS 1 ARP-GAP DOMAIN.
 [3]
 SIMILARITY: CONTRAINS 1 PH DOMAIN.

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DR EMBL: AJ243418; -, NOT_ANNOTATED_CDS.
DR HSSP: P35222; IG3J.
DR MGD: MGI:109620; Arvcf.
DR InterPro: IPR000225; Armadillo.
DR Pfam: PF00514; Armadillo_seg; 6.
DR SMART: SM00185; ARM; 4.
DR PROSITE: PSS0176; ARM_REPEAT; 3.
KW Cell adhesion; Cytoskeleton; Structural protein; Repeat; Coiled coil.
FT DOMAIN 1 39 COILED COIL (POTENTIAL).
FT NON_TER 1 1
FT REPEAT 328 376 ARM 1.
FT REPEAT 377 418 ARM 2.
FT REPEAT 419 462 ARM 3.
FT REPEAT 463 503 ARM 4.
FT REPEAT 521 560 ARM 5.
FT REPEAT 570 616 ARM 6.
FT REPEAT 634 674 ARM 7.
FT REPEAT 675 720 ARM 8.
FT REPEAT 721 769 ARM 9.
FT REPEAT 770 814 ARM 10.
SQ SEQUENCE 969 AA; 105378 MW; 91130069E484C5B5 CRC64;

Query Match 49.4%; Score 38; DB 1; Length 969;
Best Local Similarity 61.5%; Pred. NO. 1.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 2 NFAGIEAASAIQ 14
Db 664 NFNTLEAAGALQ 676

Search completed: July 3, 2003, 14:05:52
Job time: 7.5 secs

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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:03:50 ; Search time 12.5 Seconds

(without alignments)
115.361 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77
Sequence: 1 WNFAGIEAASAIQG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	95	2 A70803	early secretory an
2	47	61.0	714	2 G86844	hypothetical prote
3	44	57.1	225	2 T50707	urease accessory p
4	43	55.8	476	2 S71360	noea protein - Rhl
5	43	55.8	476	2 H95313	Noea host specific
6	42.5	55.2	141	2 H83229	conserved hypothet
7	42	54.5	369	2 E86554	Fe-S oxidoreductas
8	42	54.5	369	2 G72069	conserved hypothet
9	41	53.2	384	2 A69622	ferriochrome ABC tr
10	41	53.2	445	2 D82342	probable cadaverin
11	41	53.2	540	2 F86745	ABC transporter pe
12	40	51.9	294	2 I41220	glyceralddehyde-3-P
13	40	51.9	323	2 B97457	BH305 conserved h
14	40	51.9	323	2 AD2675	conserved hypothet
15	40	51.9	330	2 H69020	probable Na+/Ca2+
16	40	51.9	493	2 F95940	probable xanthine
17	40	51.9	536	2 B84349	hypothetical prote
18	40	51.9	761	2 T51912	hypothetical prote
19	39	50.6	101	2 F71059	hypothetical prote
20	39	50.6	287	2 B71063	hypothetical prote
21	39	50.6	379	2 S58457	ubiquinol-cytochro
22	39	50.6	379	2 S58457	ubiquinol-cytochro
23	39	50.6	445	2 B65221	probable amino aci
24	39	50.6	445	2 A91266	probable amino aci
25	39	50.6	445	2 F86106	probable amino aci
26	39	50.6	445	2 AF1022	probable amino aci
27	39	50.6	448	2 T05591	tyrosine transamin
28	39	50.6	715	2 B83518	pimeloyl-CoA synth
29	39	50.6	745	2 B33856	hypothetical 80K p

30	39	50.6	990	1 TOEC26	transposase - Esch
31	38	49.4	95	2 T10031	early secretory an
32	38	49.4	98	2 A75393	conserved hypothet
33	38	49.4	195	2 T36975	hypothetical prote
34	38	49.4	219	2 AG2036	hypothetical prote
35	38	49.4	303	2 A12211	hypothetical prote
36	38	49.4	313	2 B98234	hypothetical prote
37	38	49.4	313	2 AB3052	hypothetical prote
38	38	49.4	399	2 F87356	hypothetical prote
39	38	49.4	422	2 T05392	tyrosine transamin
40	38	49.4	422	2 S69796	pectate lyase (EC
41	38	49.4	443	2 AE0826	probable cadaverin
42	38	49.4	444	2 A41842	lysine/cadaverine
43	38	49.4	444	2 B91268	transport protein
44	38	49.4	444	2 H86108	transport of lysin
45	38	49.4	444	2 AE0147	probable amino aci

ALIGNMENTS

RESULT 1
A70803
early secretory antigen target esat6 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: A70803; S49174
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70803
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-95 <COL>
A:Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAAL1967.1; PID:el26
A:Experimental source: strain H37RV
R:Soerensen, A.L.; Nagai, S.; Houen, G.; Andersen, P.; Andersen, A.B.
submitted to the EMBL Data Library, June 1994
A:Reference number: S49174
A:Accession: S49174
A:Molecule type: DNA
A:Residues: 1-13,'R',15-22,'S',24-95 <SOE>
A:Cross-references: EMBL:X79562; NID:9531708
C:Genetics:
A:Gene: esat6

Query Match 100.0% Score 77; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIQG 15
|||||
Db 6 WNFAGIEAASAIQG 20

RESULT 2
G86844
hypothetical protein glnp [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: G86844
R:Boletín, A.; Wincker, P.; Manger, S.; Jallón, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: AB6625; MUID:21235186; PMID:11337471
A:Accession: G86844
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-714 <STO>

A:Cross-references: GB:AE005176; PID:g12724781; PIDN:AAK05857.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: glpP

Query Match 61.0%; Score 47; DB 2; Length 714;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAIQ 14
Db 303 WNFIEGFAAVDSVQ 316

RESULT 3

urease accessory protein D [Imported] - Rhodobacter sphaeroides
C:Species: Rhodobacter sphaeroides
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50707
R:Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2
A:Reference number: 225222; MUID:20115911; PMID:10648776
A:Accession: T50707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-225 <CHO>
A:Cross-references: EMBL:AF195122; PIDN:AAF24251.1
A:Experimental source: strain 2.4.1
C:Genetics:
A:Gene: ured

Query Match 57.1%; Score 44; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 4.5;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 AGIEAASAIQ 15
Db 178 AGVEAASAFDQ 189

RESULT 4

noea protein - Rhizobium meliloti
C:Species: Rhizobium meliloti
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C:Accession: S71360
R:Ardourel, M.; Lorent, G.; Maillet, F.; Roche, P.; Truchet, G.; Prome, J.C.; Rosenberg,
submitted to the EMBL Data Library, May 1995
A:Reference number: S71360
A:Accession: S71360
A:Molecule type: DNA
A:Residues: 1-476 <ARD>
A:Cross-references: EMBL:U06430; NID:g1326068; PIDN:AAK44091.1; PID:g1326070
A:Experimental source: strain RCR2011
R:Ardourel, M.; Lorent, G.; Maillet, F.; Roche, P.; Truchet, G.; Prome, J.C.; Rosenberg,
Mol. Microbiol. 17, 687-699, 1995
A:Title: In Rhizobium meliloti, the operon associated with the nod box n5 comprises nod
A:Reference number: S71357; MUID:96111489; PMID:8801423
A:Accession: S71358
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 304-339 <ARW>
A:Cross-references: EMBL:U06430
A:Experimental source: strain RCR2011 (-SU47)
C:Genetics:
A:Gene: noea
C:Superfamily: Rhizobium meliloti noea protein
C:Keywords: nodulation

Query Match 55.8%; Score 43; DB 2; Length 476;

Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAAM 10
Db 101 WSPFAGLKAAA 110

RESULT 5

Noea host specific nodulation protein [Imported] - Sinorhizobium meliloti (strain 102
H95313
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: H95313
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium mel
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95313
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65074.1; PID:g14523508; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: noea
A:Genome: plasmid
C:Superfamily: Rhizobium meliloti noea protein

Query Match 55.8%; Score 43; DB 2; Length 476;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAAM 10
Db 101 WSPFAGLKAAA 110

RESULT 6

conserved hypothetical protein PA3332 [Imported] - Pseudomonas aeruginosa (strain PAO
H83229
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83229
R:Stover, C.K.; Yam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: A82950; MUID:20457337; PMID:10984043
A:Accession: H83229
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <STO>
A:Cross-references: GB:AE004755; GB:AE004091; NID:g9949456; PIDN:ANG06720.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA3332
C:Superfamily: Bacillus subtilis hypothetical protein yese

Query Match 55.2%; Score 42.5; DB 2; Length 141;
Best Local Similarity 40.9%; Pred. No. 5.1;
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

QY 1 WN-----FAGIEAASAI0G 15
||| ||| ||| |||
DB 119 WNPJRHLEALGCGVEAAKIV0G 140

RESULT 7

Re-S oxidoreductase [imported] - Chlamydia pneumoniae (strain J138)
E86554
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86554
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishl, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86554
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-369 <STO>
A:Cross-references: GB:BA000008; NID:98978883; PIDN:BA98719.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0513
C:Superfamily: hypothetical protein AF0390

Query Match 54.5%; Score 42; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAA 9
||| ||| ||| |||
DB 305 WNYLGIEAA 313

RESULT 8

Conserved hypothetical protein CP0240 [imported] - Chlamydia pneumoniae (strains CML
G72069
N:Alternate names: fe-s oxidoreductase
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: G72069; F81599
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Ollinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: G72069
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-369 <ARR>
A:Cross-references: GB:AE001636; GB:AE001363; NID:94376794; PIDN:AA018653.1; PID:9437680
A:Experimental source: strain CML029
R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: F81599
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-369 <REA>
A:Cross-references: GB:AE002184; GB:AE002161; NID:97189156; PIDN:AAF8105.1; PID:9718916
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CPN0513; CP0240
C:Superfamily: hypothetical protein AF0390

Query Match 54.5%; Score 42; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAA 9
||| ||| ||| |||

DB 305 WNYLGIEAA 313

RESULT 9

ferrichrome ABC transporter (permease) fhvB - Bacillus subtilis
A69622
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: A69622
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
lechi, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardio
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y. M.; Ogawa, K.; Ogilawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rooha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A:Authors: Schleib, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchida
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69622
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-384 <KUN>
A:Cross-references: GB:299121; GB:AL009126; NID:92635827; PIDN:CAB15337.1; PID:926358
A:Experimental source: strain 168
C:Genetics:
A:Gene: fhvB
C:Superfamily: vitamin B12 transport protein btuc

Query Match 53.2%; Score 41; DB 2; Length 384;
Best Local Similarity 46.7%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 WNFAGIEAASAI0G 15
||| ||| ||| |||
DB 174 WSFAGAGLGAATVWG 188

RESULT 10

Probable cadaverine/lysine antiporter CadB VC0280 [imported] - Vibrio cholerae (strai
DB2342
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: DB2342
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
Chardson, D.; Ermolaeva, M.D.; Vamthanan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: DB2342
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-445 <HEI>
A:Cross-references: GB:AE004116; GB:AE003852; NID:99654687; PIDN:AAF93455.1; GSPDB:GN
A:Experimental source: serogroup O1, strain N16961, biotype El Tor
C:Genetics:
A:Gene: VC0280
A:Map position: 1
C:Superfamily: L-lysine transport protein

Query Match 53.2%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNFAGIEAANA 10
||| ||| ||| |||

Db 199 MSFVGVESA 208

RESULT 11

ABC transporter permease protein yj1D [Imported] - Lactococcus lactis subsp. lactis (str F86745)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: F86745
 R:Holotin, A.; Winkler, P.; Mueger, S.; Jalllon, O.; Malarme, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: F86745
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-540 <STO>
 A:Cross-references: GB:AE005176; PID:g12723906; PIDN:AAK05064.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: yj1D

Query Match 53.2%; Score 41; DB 2; Length 540;
 Best Local Similarity 69.2%; Pred. No. 37;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 FAGIEAASAI06 15
 Db 339 FVGNETASAI06 351

RESULT 12

glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Escherichia h
 C:Species: Escherichia blattae
 C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 03-Jun-2002
 C:Accession: I41220; I41223; I41226
 R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J. Gen. Microbiol. 137, 1911-1921, 1991
 A:Title: Molecular and evolutionary relationships among enteric bacteria.
 A:Reference number: I40701; MUID:92065252; PMID:1955870
 A:Accession: I41220
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-294 <RES>
 A:Cross-references: GB:M63358; NID:g146076; PIDN:AAA23837.1; PID:g146077
 A:Accession: I41223
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-294 <RES>
 A:Cross-references: GB:M63359; NID:g146108; PIDN:AAA23852.1; PID:g146109
 A:Experimental source: ATCC 33429
 A:Accession: I41226
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-294 <RES>
 A:Cross-references: GB:M63360; NID:g146114; PIDN:AAA23855.1; PID:g146115
 A:Experimental source: ATCC 33430
 C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C:Keywords: oxidoreductase

Query Match 51.9%; Score 40; DB 2; Length 294;
 Best Local Similarity 58.3%; Pred. No. 29;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 WNFAGIEAASA 12
 Db 70 WNEAGIEVAAE 81

RESULT 13

B97457
 BH3305 conserved hypothetical [Imported] - Agrobacterium tumefaciens (strain C58, Cereon

C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: B97457

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldm
 A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2333-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
 A:Reference number: A97359; PMID:11743194
 A:Accession: B97457
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-323 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK86611.1; PID:g15155783; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C1468
 A:Map position: circular chromosome

Query Match 51.9%; Score 40; DB 2; Length 323;
 Best Local Similarity 61.5%; Pred. No. 32;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 FAGIEAASAI06 15
 Db 11 FAGISCAATPALAG 23

RESULT 14

conserved hypothetical protein Atu0802 [Imported] - Agrobacterium tumefaciens (strain
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AD2675
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gallet, W.; Grant, C.; Guehner, D.; Kuyavin, T.; Levy, R.; Li, M.; McCl
 science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AD2675
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-323 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAI41818.1; PID:g17739175; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu0802
 A:Map position: circular chromosome

Query Match 51.9%; Score 40; DB 2; Length 323;
 Best Local Similarity 61.5%; Pred. No. 32;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 FAGIEAASAI06 15
 Db 11 FAGISCAATPALAG 23

RESULT 15

probable Na⁺/Ca²⁺-K⁺-exchanging protein - Methanobacterium thermoautotrophicum (strai
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: H69020
 R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T
 ; Qiu, D.; Spadofora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
 K.I.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: H69020
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-330 <MTH>
A:Cross-references: GB:AE000885; GB:AE000666; NID:g2622256; PIDN:AA885644.1; PID:g262226
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH155
A:Start codon: TTG

Query Match 51.9%; Score 40; DB 2; Length 330;
Best Local Similarity 46.7%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 WNFAGIEPAASAIQG 15
||| | : | : |
DB 95 WNIAGILGISSVAG 109

Search completed: July 3, 2003, 14:07:19
Job time : 13.5 secs

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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:00:24 ; Search time 30 Seconds

(without alignments)
66.625 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 MNFAGIEAASAIQIG 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1995.DAT:*
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18: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1997.DAT:*
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20: /SIDS2/gcgdata/geneseq/genesep-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/genesep-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	21	AAV94595
2	77	100.0	15	23	AAO17433
3	77	100.0	20	22	AAE12275
4	77	100.0	51	18	AAW32466
5	77	100.0	51	18	AAW32339
6	77	100.0	51	19	AAW81701
7	77	100.0	51	19	AAW64334
8	77	100.0	51	20	AAV39131
9	77	100.0	51	20	AAV38988
10	77	100.0	51	22	AAU01897

11	77	100.0	51	23	AAE17580	Mycobacterium spec
12	77	100.0	95	16	AAW11494	ESAT-6, Mycobacter
13	77	100.0	95	20	AAV29890	Mycobacterium tube
14	77	100.0	95	20	AAV29788	Mycobacterium tube
15	77	100.0	95	22	AAV35219	M tuberculosis RV3
16	77	100.0	95	23	AAW50740	Mycobacterium tube
17	77	100.0	196	20	AAV29888	Mycobacterium tube
18	77	100.0	403	19	AAW72943	Mycobacterium tube
19	77	100.0	403	20	AAV21963	Amino acid sequenc
20	77	100.0	404	19	AAW72842	Mycobacterium tube
21	77	100.0	404	20	AAV21962	Amino acid sequenc
22	77	92.2	19	18	AAW35548	ESAT-6 antigen SEQ
23	66	85.7	20	22	AAE12276	Mycobacterium tube
24	62	80.5	17	21	AAV88581	Antigenic N-termin
25	60	77.9	13	22	AAE12274	Mycobacterium tube
26	54	70.1	15	21	AAV94590	Mycobacterium tube
27	54	70.1	15	23	AAO17432	Early secreted ant
28	47	61.0	714	23	ABW55108	Lactococcus lactis
29	44	57.1	15	21	AAV94599	Mycobacterium tube
30	42	54.5	409	20	AAV35136	Chlamydia pneumoni
31	41	53.2	540	23	ABW54282	Lactococcus lactis
32	40	51.9	81	22	AAU42889	Propionilbacterium
33	40	51.9	403	22	AAW40540	Human polypeptide
34	40	51.9	2293	21	AAV69197	Amino acid sequenc
35	39	50.6	9	19	AAW61077	Human OREX ORF1592
36	39	50.6	140	21	AAW41828	Human polypeptide
37	39	50.6	162	22	AAW40271	Human polypeptide
38	39	50.6	162	22	AAW93538	Human protein sequ
39	39	50.6	162	22	AAV72606	Human Electon tra
40	39	50.6	209	21	AAW36643	Arabidopsis thalia
41	39	50.6	221	21	AAV91434	Human secreted pro
42	39	50.6	228	22	AAW42057	Human polypeptide
43	39	50.6	232	21	AAW36642	Arabidopsis thalia
44	39	50.6	232	22	AAU221824	Novel human neopla
45	39	50.6	253	22	AAW23550	Human EST encoded

ALIGNMENTS

RESULT 1	
AAV94595	
ID	AAV94595 standard; peptide; 15 AA.
XX	
AC	AAV94595;
DT	28-NOV-2000 (first entry)
XX	
DE	Mycobacterium tuberculosis ESAT-6 peptide ES6.
XX	
KW	Tuberculosis; infection diagnosis; ESAT-6.
XX	
OS	Mycobacterium tuberculosis.
XX	
PN	WO200026248-A2.
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99MO-GB03635.
XX	
PR	04-NOV-1998; 98GB-0024213.
PR	04-NOV-1998; 98US-0107004.
XX	
PA	(ISIS-) ISIS INNOVATION LTD.
XX	
PI	Lalvani A, Pathan AA;
XX	
DR	WPI; 2000-365579/31.
PT	Novel method of diagnosing infection, or exposure of a host, to a
PT	Mycobacterium comprising contacting T cells from the host with ESAT-6
PT	derived peptides -
XX	

PS Claim 1; Page 3; 33pp; English.
XX
CC The present sequence is the peptide ES6 derived from the Mycobacterium
CC tuberculosis ESAT-6 gene. This sequence is one of eleven peptides
CC derived from the ESAT-6 gene (see AAY94590 to AAY94600). The peptides
CC are recognized, to varying degrees, by the T cells of patients with
CC tuberculosis. When the peptides are combined together as a panel they
CC provide a high specificity and sensitivity diagnostic test for
CC M. tuberculosis infection. This test has the advantage that it does not
CC give false positives for patients who have been vaccinated with BCG.
XX
SQ Sequence 15 AA:
Query Match 100.0%; Score 77; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAASAIQG 15
DB 1 WNFAGIEAASAIQG 15
RESULT 2
AA017433
ID AA017433 standard; peptide; 15 AA.
XX
AC AA017433;
XX
DT 11-JUL-2002 (first entry)
XX
DE Early secreted antigenic target 6 T cell epitope #2.
XX
KM Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;
KM poxvirus vector; HIV; malaria; Helicobacter pylori; influenza;
KM hepatitis; viral infection; leprosy; protozoan parasite; cancer;
KM tuberculosis; anti-HIV; protozoicide; antibacterial; vituicide;
KM hepatotropic; anti-inflammatory; antileptotic; cytoskeletal; epitope.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200224224-A2.
XX
PD 28-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-GB04116.
XX
PR 21-SEP-2000; 2000GB-0023203.
XX
PA (OXO-) OXON PHARMACEUTICALS LTD.
XX
PI Hill AVS, McShane H, Gilbert S, Reece W, Schneider J;
XX
DR WPI; 2002-394098/42.
XX
PT Inducing CD4+ T-cell response against target antigen by administering a
PT composition comprising a source of CD4+ epitopes which is a
PT non-replicating or replication impaired recombinant poxvirus vector -
XX
PS Example 1; Page 21; 50pp; English.
XX
CC The present invention relates to a method of inducing a CD4+ T-cell
CC response against a target antigen, by administering two different
CC compositions comprising a source of CD4+ T-cell epitope(s) of the target
CC antigen, where the second composition further includes an epitope which
CC is same as the epitope of the first composition, where the source of the
CC epitopes for the compositions is a non-replicating or replication
CC impaired recombinant poxvirus vector. The methods are useful for inducing
CC CD4+ T-cell immune responses against diseases such as tuberculosis, human
CC immunodeficiency virus (HIV) (persistent viral infection), malaria,
CC Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
CC cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
CC leprosy and diseases caused by non-malarial protozoan parasite such as
CC toxoplasma and cancer. The present sequence is an epitope from

CC Mycobacterium tuberculosis useful in the method of the invention.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAASAIQG 15
DB 1 WNFAGIEAASAIQG 15
RESULT 3
AAE12275
ID AAE12275 standard; peptide; 20 AA.
XX
AC AAE12275;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mycobacterium tuberculosis (Mtb) peptide #60.
XX
KM Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
KM infection; anti-Mtb immune response.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200170774-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US08906.
XX
PR 20-MAR-2000; 2000US-190834P.
XX
PA (UYBR-) UNIV BROWN RES. FOUND.
XX
PI Degroot AS;
XX
DR WPI; 2001-616401/71.
XX
PT New vaccine for immunizing a mammalian subject, preferably humans,
PT against infection caused by Mycobacterium tuberculosis -
XX
PS Disclosure; Fig 4; 42pp; English.
XX
CC The present invention relates to Mycobacterium tuberculosis (Mtb)
CC vaccine candidate peptides. The invention also relates to a method
CC for identifying Mtb vaccine candidate peptides as well as vaccines
CC comprising these candidate peptides. Vaccines of the invention and
CC Mtb vaccine candidate peptides are useful for inducing an anti-
CC Mycobacterium tuberculosis (anti-Mtb) immune response by raising
CC anti-Mtb antibody in a mammalian subject preferably human. They
CC are used for immunizing a mammalian subject, preferably humans,
CC against infection caused by Mycobacterium tuberculosis. The present
CC sequence is a Mtb vaccine candidate peptide.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 77; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNFAGIEAASAIQG 15
DB 2 WNFAGIEAASAIQG 16
RESULT 4
AAW32466
ID AAW32466 standard; Protein; 51 AA.
XX

AC		AAM32466;	
XX			
DT	09-JAN-1998	(first entry)	
XX			
DE	Mycobacterium tuberculosis antigen ESAT-6.		
XX			
KM	Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.		
XX			
OS	Mycobacterium tuberculosis.		
PN	WO9709428-A2.		
XX			
PB	13-MAR-1997.		
XX			
PE	30-AUG-1996;	96WO-US14674.	
XX			
PR	12-JUL-1996;	96US-0680574.	
PR	01-SEP-1995;	95US-0523436.	
PR	22-SEP-1995;	95US-0533634.	
PR	22-MAR-1996;	96US-0620874.	
PR	05-JUN-1996;	96US-0659683.	
PA	(CORI-) CORIXA CORP.		
XX			
PI	Campos-neto A, Dillon DC, Houghton R, Reed SG, Skeiky YAM; Twardzik DR, VeeDVick TH;		
XX			
DR	WPI: 1997-192903/17. N-PADB: AAP91529.		
PT	New Immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also for diagnosis		
PS	Disclosure; Page 135; 168pp; English.		
CC			
CC	A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, ESAT-6. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or prevention).		
SQ	Sequence	51 AA:	
	Query Match	100.0%;	Score 77; DB 18; Length 51;
	Best Local Similarity	100.0%;	Pred. No. 5.2e-06;
	Matches	15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MNFAGIEAAASAIOG	15	
ID			
DB	6 MNFAGIEAAASAIOG	20	
RESULT 5			
AAM32339	AAM32339 standard; Protein; 51 AA.		
AC	AAM32339;		
DT	13-JAN-1998	(first entry)	
DE	Mycobacterium tuberculosis antigen ESAT-6.		
KM	Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.		
OS	Mycobacterium tuberculosis.		

```
PN MW0709429-A2.  
XX  
PD 13-MAR-1997.  
XX  
PF 30-AUG-1996;    96WO-USI4675.  
XX  
PR 12-JUL-1996;     96US-0680573.  
PR 01-SEP-1995;      95US-0523435.  
PR 22-SEP-1995;      95US-0532136.  
PR 22-MAR-1996;       96US-0620280.  
PR 05-JUN-1996;        96US-0658800.  
XX  
PA (CORI-) CORIXA CORP.  
XN Campos-neto A., Dillon DC, Houghton R, Reed SG, Skelky YAW;  
PI Twardzik DR, Vedvick TH,  
XX WPI: 1997-192904/17.  
DR N-PSTDB; AAT91463.  
XX  
PT New immunogenic polypeptide(s) from soluble M. tuberculosis antigens  
PT - useful for diagnosis of M. tuberculosis infection  
XX  
PS Claim 43; Page 147; 190pp; English.  
XX A new immunogenic polypeptide has been developed comprising an  
CC immunogenetic part of a soluble Mycobacterium tuberculosis antigen (or  
CC its variant differing only in conservative substitutions and/or  
CC modifications). The present sequence represents a specifically claimed  
CC sequence of the ESAT-6 M.tuberculosis antigen. The Immunogenic  
CC polypeptide can be used to diagnose M.tuberculosis infection by forming  
CC complexes with specific antibodies in the sample. Fragments of DNA  
CC encoding the immunogenic polypeptide can be used as diagnostic primers  
CC or probes and agents that bind to the antigen, especially monoclonal  
CC antibodies or equivalent polyclonal antibodies, are also used for  
CC diagnosis.  
CX  
SX Sequence   51 AA:  
SO  
  
Query Match           100.0%; Score 77; DB 18; Length 51;  
Best Local Similarity 100.0%; Pred. No. 5.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY             1 MNFAGIEAAASAIQG 15  
                |||  
Db              6 MNFAGIEAAASAIQG 20  
  
RESULT 6  
AAW81701  
ID AAW81701 standard; Protein; 51 AA.  
AC AAW81701;  
XX  
DT 27-JAN-1999 (first entry)  
.xx  
DE M. tuberculosis immunogenic polypeptide ESAT-6.  
KW Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;  
KV vaccine; pharmaceutical; infection; diagnosis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WC9816646-A2.  
XX  
PD 23-APR-1998.  
PE 07-OCT-1997;    97WO-USI8293.  
PX 13-MAR-1997;    97US-0818112.  
PR 11-OCT-1996;    96US-0730510.  
PA (CORI-) CORIXA CORP.
```

XX Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
 PI Reed SG, Skeiky YAM, Twardzik DR, Vedvick TS;
 XX WPI: 1998-261042/23.
 DR N-PSDB: AAV64501.
 XX
 PT Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used
 PT to develop products for the detection of M. tuberculosis infection
 PT and for diagnosis, treatment and prevention of tuberculosis
 XX
 PS Disclosure; Page 126; 230pp; English.
 XX
 CC This sequence represents an immunogenic portion of a soluble
 CC Mycobacterium tuberculosis (MT) antigen which can be used in a method
 CC for inducing protective immunity against tuberculosis (TB). This
 CC sequence can be formulated into vaccines and/or pharmaceutical
 CC compositions for immunising against M. tuberculosis infection or may
 CC be used for the diagnosis of tuberculosis.
 CC
 SQ Sequence 51 AA:
 Query Match 100.0%; Score 77; DB 19; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WNFAGIEAASAIQG 15
 Db 6 WNFAGIEAASAIQG 20
 XX
 RESULT 7
 AAW64334
 ID AAW64334 standard; Protein; 51 AA.
 XX
 AC AAW64334;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Mycobacterium tuberculosis antigen ESAT-6.
 XX
 KM Tuberculosis; infection; diagnosis; antigen; ESAT-6.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN W09816645-A2.
 XX
 PD 23-APR-1998.
 XX
 PE 07-OCT-1997; 97WO-US18214.
 XX
 PR 13-MAR-1997; 97US-0818111.
 PR 11-OCT-1996; 96US-0729622.
 XX
 PA (CORT-) CORIXA CORP.
 XX
 PI Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
 PI Reed SG, Skeiky YAM, Twardzik DR, Vedvick TS;
 XX WPI: 1998-251292/22.
 DR N-PSDB: AAV44393.
 XX
 PT New isolated Mycobacterium tuberculosis polypeptides and DNA - used
 PT to develop products for the detection of M. tuberculosis infection
 PT and diagnosis of tuberculosis
 XX
 PS Disclosure; Page 130; 250pp; English.
 XX
 CC This polypeptide comprises an antigenic portion of Mycobacterium
 CC tuberculosis antigen ESAT-16. The invention relates to
 CC compositions and methods for diagnosing tuberculosis. It provides
 CC polypeptides (see AAW64291-W64379) comprising an antigenic portion
 CC of a soluble M. tuberculosis antigen, or an immunogenic portion of

CC an M. tuberculosis antigen, as well as fusion proteins between
 CC these polypeptides and known antigens such as ESAT-6. Also claimed
 CC are methods and diagnostic kits for detecting M. tuberculosis
 CC infection in a patient using these polypeptides, antibodies, or
 CC oligonucleotide probes and primers.
 CC
 SQ Sequence 51 AA:
 Query Match 100.0%; Score 77; DB 19; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WNFAGIEAASAIQG 15
 Db 6 WNFAGIEAASAIQG 20
 XX
 RESULT 8
 AAY39131
 ID AAY39131 standard; Protein; 51 AA.
 XX
 AC AAY39131;
 XX
 DT 05-NOV-1999 (first entry)
 XX
 DE M. tuberculosis ESAT-6 amino acid sequence.
 XX
 KM Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
 KM immunotherapy; diagnosis; immunisation; vaccine; infection;
 KM immune response; skin test.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN W09942076-A2.
 XX
 PD 26-AUG-1999.
 XX
 PE 17-FEB-1999; 99WO-US03268.
 XX
 PR 05-MAY-1998; 98US-0072967.
 PR 18-FEB-1998; 98US-0025197.
 XX
 PA (CORT-) CORIXA CORP.
 XX
 PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAM, Twardzik DR, Vedvick TS;
 XX WPI: 1999-527409/44.
 DR N-PSDB: AA219303.
 XX
 PT New antigens from Mycobacterium tuberculosis useful in diagnostic
 PT skin tests and protective or therapeutic vaccines or compositions
 XX
 PS Disclosure; Page 120; 299pp; English.
 XX
 CC The present invention describes polypeptides comprising an immunogenic
 CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
 CC are vaccines and fusion protein containing M. tuberculosis Ag's.
 CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
 CC other polypeptides fragments, can be used in pharmaceutical compositions
 CC or vaccines to generate a protective or therapeutic immune response to
 CC M. tuberculosis and as reagents in skin tests for diagnosis of
 CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
 CC by, T, B or natural killer cells and/or macrophages in
 CC tuberculosis-immune subjects. AA219249 to AA219460 and AAY39083 to
 CC AAY39225 are used in the exemplification of the present invention.
 CC
 SQ Sequence 51 AA:
 Query Match 100.0%; Score 77; DB 20; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI0G 15
 |||||
 DB 6 WNFAGIEAASAI0G 20

RESULT 9
 ID AAY38988 standard; Protein: 51 AA.

XX AAY38988;

DT 05-NOV-1999 (first entry)

DE M. tuberculosis recombinant antigen protein ESAT-6.

KW Antigen; diagnosis; detection; infection; antibody; immunisation;
 KM vaccine; immunity.

OS Mycobacterium tuberculosis.

PN W09942118-A2.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US03265.

PR 05-MAY-1998; 98US-0072596.

PR 18-FEB-1998; 98US-0024753.

PA (CORI-) CORIXA CORP.

PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 Lodes MJ, Reed SG, Skeiky YAM, Twardzik DR, VEDVICK TS;

DR WPI: 1999-527416/44.

DR N-PSDB: AAZ19091.

PT New polypeptide comprising antigenic portions of M. tuberculosis

PS Claim 51; Page 165; 323pp; English.

CC This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against
 CC M. tuberculosis infection. The new detection methods are needed as
 CC current vaccination strategies do not provide 100% immunity.

SO Sequence 51 AA;

Query Match 100.0%; Score 77; DB 20; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI0G 15
 |||||
 DB 6 WNFAGIEAASAI0G 20

RESULT 10
 ID AAU01897 standard; Protein: 51 AA.

XX AAU01897;

DT 29-AUG-2001 (first entry)

DE Mycobacterium tuberculosis partial antigen ESAT-6.

KW ESAT-6; antigen; vaccine; tuberculosis; AIDS;
 KM acquired immunodeficiency disease.

XX

OS Mycobacterium tuberculosis.

PN W0200124820-A1.

PD 12-APR-2001.

PF 10-OCT-2000; 2000WO-US28095.

PR 07-OCT-1999; 99US-0158338.

PR 07-OCT-1999; 99US-0158425.

PA (CORI-) CORIXA CORP.

PI Skeiky Y, Reed S, Houghton RL, McNeill PD, Dillon DC, Lodes MJ;

DR WPI: 2001-290576/30.

DR N-PSDB: AAS03787.

PT Vaccinating against Mycobacteria infections in mammals using fusion
 proteins comprising combinations of heterologous antigens

PS Disclosure: Page 164; 168pp; English.

CC The sequence represents Mycobacterium tuberculosis ESAT-6 antigen.
 CC Compositions comprising at least 2 heterologous antigens, as a fusion
 CC protein, and vectors expressing the fusion proteins are used as vaccines
 CC to prophylactically immunise mammals (especially humans) against
 CC infection by Mycobacteria. The compositions contain at least 2
 CC heterologous antigens that increase the serological sensitivity of
 CC individuals infected with tuberculosis, a disease frequently affecting
 CC patients with acquired immunodeficiency disease, AIDS.

SO Sequence 51 AA;

Query Match 100.0%; Score 77; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNFAGIEAASAI0G 15
 |||||
 DB 6 WNFAGIEAASAI0G 20

RESULT 11
 ID AAE17580 standard; Protein: 51 AA.

XX AAE17580;

DT 22-APR-2002 (first entry)

DE Mycobacterium species ESAT-6 protein.

KW Fusion protein; antigen; serological sensitivity; immune response;
 KM tuberculosis; infection; vaccine; ESAT-6 protein.

OS Mycobacterium sp.

PN W0200198460-A2.

PD 27-DEC-2001.

PF 20-JUN-2001; 2001WO-US19959.

PR 20-JUN-2000; 2000US-0597796.

PR 01-FEB-2001; 2001US-265737P.

PA (CORI-) CORIXA CORP.

PI Skeiky Y, Reed S, Alderson M;

DR WPI: 2002-147798/19.

DR N-PSDB: AAD28351.

XX Composition comprising MTB39 antigen and MTB32A antigen from
PT Mycobacterium species, useful for eliciting immune response in a
PT subject
XX
XX Claim 9; Page 122; 136pp; English.
XX
XX The present invention relates to fusion proteins containing at least
CC two Mycobacterium species antigens, nucleotides encoding them and
CC compositions comprising such fusion proteins. The present invention
CC particularly relates to nucleic acids encoding fusion proteins that
CC include two or more individual M. tuberculosis antigens which increase
CC the serological sensitivity of sera from individuals infected with
CC tuberculosis and methods for their use in diagnosis, prevention and
CC treatment of tuberculosis infection. Sequences of the invention are
CC useful for eliciting an immune response in a mammal, e.g., human,
CC immunised with BCG. They are useful in the diagnosis, treatment and
CC prevention of Mycobacterium infection. The fusion proteins and the
CC polynucleotides are useful as diagnostic tools in patients infected
CC with Mycobacterium, in vitro and in vivo assays for detecting humoral
CC antibodies or cell-mediated immunity against M. tuberculosis, for the
CC diagnosis of an infection or monitoring of disease progression, as
CC immunogens to generate or elicit a protective immune response in a
CC patient and for raising anti-M. tuberculosis antibodies in a non-human
CC animal. Sequences of the invention are also used as vaccines. MTB32A
CC fusion proteins of the invention are useful as in vivo diagnostic agents
CC for intradermal skin test. The present sequence is Mycobacterium species
CC ESAT-6 protein.
CC
XX
SO Sequence 51 AA:

Query Match 100.0%; Score 77; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 5,2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFAGIEAASAIQG 15
| | | | | | | | | | | | | | | | | | | | |
DB 6 MNFAGIEAASAIQG 20

RESULT 12
AAW11494
ID AAW11494 standard; Protein; 95 AA.
XX
XX AAW11494;
AC
XX
XX
XX 27-MAR-1997 (first entry)
DE
XX
XX ESAT6.
XX
XX
XX ESAT6; Mycobacterium tuberculosis; 6kda antigen; tuberculosis complex;
KM HVB76-8 reactive antigen; interferon-gamma; memory T-lymphocyte; vaccine;
KM M. africanum; M. bovis; delayed-type hypersensitivity reaction; therapy.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX W09501441-A1.
PN
XX
XX 12-JAN-1995.
PD
XX
XX 01-JUL-1994; 94MO-DK00273.
PF
XX
XX 02-JUL-1993; 93DK-0000798.
PR
XX
XX (STAT-) STATENS SERUMSINSTITUT.
PA
XX
XX Andersen AB, Andersen P, Haslov K, Sorensen A;
PI
XX
XX WPI; 1995-061005/08.
DR
XX
XX N-PSDB; AAT51422.
DR
XX
XX Vaccine for tuberculosis induces interferon-gamma release from
PT T-lymphocytes - comprises an antigen released from mycobacteria,

PT for immunisation of humans
XX
XX Claim 5; Page 61-63; 101pp; English.
XX
XX This sequence represents the Mycobacterium tuberculosis ESAT6. ESAT6 is
CC also known as the 6kda antigen, or the HVB76-8 reactive antigen. ESAT6
CC is released from metabolising bacteria, and can be isolated from short
CC term filtrates grown as shaken cultures for 7 days. ESAT6 also induces a
CC release of interferon-gamma from reactivated memory T-lymphocytes. This
CC protein sequence is included in the vaccine of the invention. The
CC vaccine is for immunising an animal (including humans) against
CC tuberculosis caused by a Mycobacteria belonging to the tuberculosis
CC complex. The Mycobacteria of the tuberculosis complex are, M.
CC tuberculosis, M. africanum, and M. bovis. The vaccine can evoke a
CC protective immune response against tuberculosis or a delayed-type
CC hypersensitivity reaction. The protein can also be included in a
CC composition for diagnosing tuberculosis. The composition is injected
CC intradermally, and a skin reaction is an indicator of tuberculosis.
XX
XX
SO Sequence 95 AA:

Query Match 100.0%; Score 77; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFAGIEAASAIQG 15
| | | | | | | | | | | | | | | | | | | | |
DB 6 MNFAGIEAASAIQG 20

RESULT 13
AAZ29890
ID AAZ29890 standard; Protein; 95 AA.
XX
XX AAZ29890;
AC
XX
XX
XX 18-NOV-1999 (first entry)
DT
XX
XX
XX Mycobacterium tuberculosis ESAT-6 protein sequence.
DE
XX
XX Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
KM delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
KM interferon-gamma release.
XX
XX
XX Mycobacterium tuberculosis.
OS
XX
XX W09945119-A2.
PN
XX
XX 10-SEP-1999.
PD
XX
XX 05-MAR-1999; 99MO-DK00109.
PF
XX
XX 06-MAR-1998; 98DK-0000306.
PR
XX
XX 06-MAR-1998; 98US-0077105.
PR
XX
XX (STAT-) STATENS SERUM INST..
PA
XX
XX Jensen CL, Folkersen J;
PI
XX
XX WPI; 1999-551043/46.
DR
XX
XX N-PSDB; AAZ21132.
DR
XX
XX New mycobacterial polypeptide produced in lactic acid bacteria, useful
PT in tuberculosis diagnosis and vaccines
PT
XX
XX Disclosure; Page 75-76; 76pp; English.
XX
XX The present invention describes a bioactive polypeptide (or
CC immunologically equivalent analogue) produced in lactic acid bacteria
CC which reacts with lymphoid cells primed with Mycobacterium tuberculosis
CC complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The
CC polypeptide and ESAT-6 polypeptides are useful in compositions for
CC diagnosis of and vaccination against tuberculosis caused by

CC M. tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used
CC to diagnose ongoing/previous sensitization with these bacteria by
CC detecting cytokine release when contacting blood samples with the
CC polypeptide. The bioactive polypeptide may be used in diagnostic
CC compositions and vaccines for mycobacteria other than of the
CC M. tuberculosis complex, e.g. M. avium which infects poultry and
CC occasionally humans, M. leprae; they are especially useful when they do
CC not react with lymphoid cells previously primed with M. tuberculosis
CC complex mycobacteria, and so do not give rise to a diagnostic reaction
CC in individuals infected with these bacteria. The polypeptides may also
CC be used in in vitro diagnostic tests e.g. stimulation of interferon-gamma
CC release from lymphocytes. The polypeptide has similar or higher
CC bioactivity as currently used tuberculin reagent in the standard
CC delayed type hypersensitivity (DTH) skin test for tuberculosis, but may
CC have greater specificity, being better able to discriminate between
CC lymphoid cells primed from tuberculosis and from previous vaccination.
CC The present sequence represents M. tuberculosis ESAT-6 used in the
CC exemplification of the present invention.

XX Sequence 95 AA;

Query Match 100.0%; Score 77; DB 20; Length 95;

Best Local Similarity 100.0%; Pred. No. 1e-05; Mismatches 0; Indels 0; Gaps 0;

DB 1 WNFAGIEAASAIQG 15
6 WNFAGIEAASAIQG 20

RESULT 14

AA29788 standard; Protein; 95 AA.

XX AAY29788;

XX 08-NOV-1999 (first entry)

XX Mycobacterial tuberculosis ESAT-6 protein.

XX Mycobacterial; ESAT-6; 6 kDa antigen; tuberculosis; infection;

XX Immunological response; diagnosis; vaccine.

XX Mycobacterium tuberculosis.

XX US9595077-A.

XX 21-SEP-1999.

XX 05-JUN-1995; 95US-0465640.

XX 05-JUN-1995; 95US-0465640.

XX 20-SEP-1993; 93US-0123182.

XX 01-JUL-1994; 94WO-DK00273.

XX (STAT-) STATENS SERUMINSTITUT.

XX Andersen AB, Andersen P, Haslov K, Sorensen AL;

XX WPI, 1999-539545/45.

XX N-PSDB; AA208877.

XX Polypeptide secreted from Mycobacterium is useful as a vaccine

XX against tuberculosis

XX Claim 24; Fig 10C; 39pp; English.

XX The present invention describes a purified or non-naturally occurring

CC polypeptide (I) released from a metabolizing mycobacteria comprising an

CC ESAT-6, also called the 6 kDa antigen. The present sequence represents an

CC Mycobacterium tuberculosis ESAT-6 protein. Also described is a purified

CC or non-naturally occurring polypeptide (II) with the ability to elicit

CC a delayed type hypersensitivity reaction which comprises a T cell

CC epitope of (I). (II) can be used with a carrier or vehicle in a
CC composition for diagnosing tuberculosis caused by mycobacteria belonging
CC to the tuberculosis complex, i.e. Mycobacterium tuberculosis, M. bovis
CC and M. africanum. The composition can be used to detect microbial
CC antibodies or components of mycobacteria in samples or in animals
CC through the use of immunoassays. (II) can be used as a vaccine for
CC immunizing an animal, including humans against tuberculosis caused by
CC mycobacteria of the tuberculosis-complex. (II) induce a release of
CC IFN-gamma from reactivated T-lymphocytes evoking a protective immune
CC response. Vaccine containing (II) has the same protective potency as
CC the live BCG vaccine against tuberculosis.

XX Sequence 95 AA;

Query Match 100.0%; Score 77; DB 20; Length 95;

Best Local Similarity 100.0%; Pred. No. 1e-05; Mismatches 0; Indels 0; Gaps 0;

DB 1 WNFAGIEAASAIQG 15
6 WNFAGIEAASAIQG 20

RESULT 15

AAB35219 standard; Protein; 95 AA.

XX AAB35219;

XX 24-APR-2001 (first entry)

XX M tuberculosis RV3875 protein.

XX Tuberculosis; TB; vaccine; esat-6 gene family; RV0287; RV1036C;

XX RV1037C; RV2346C; RV2348C; RV2653C; RV3020C; RV3444C;

XX RV3445C; RV3890C; RV3891C; RV3904C; RV3905C.

XX Mycobacterium tuberculosis.

XX WO200104151-A2.

XX 13-JUL-2000; 2000WO-DK00398.

XX 13-JUL-1999; 99DK-0001020.

XX 15-JUL-1999; 99US-0144011.

XX (STAT-) STATENS SERUM INST.

XX Andersen P, Skjot R;

XX WPI, 2001-091923/10.

XX New polypeptide encoded by a member of the esat-6-gene family for

XX immunizing against and diagnosis of tuberculosis -

XX Example 2; Page 65; 80pp; English.

XX The present invention provides the protein and coding sequences for

XX members of the esat-6 gene family from Mycobacterium tuberculosis. These

XX proteins include RV0287, RV1037C, RV2346C, RV2348C, RV2653C,

XX RV2654C, RV3020C, RV3444C, RV3445C, RV3890C, RV3891C, RV3904C and

XX RV3905C. These can be used to produce vaccines against, and in the

XX diagnosis of, tuberculosis (TB) infection. The present sequence is one of

XX the proteins of the invention.

XX Sequence 95 AA;

Query Match 100.0%; Score 77; DB 22; Length 95;

Best Local Similarity 100.0%; Pred. No. 1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:05:35 ; Search time 17.5 Seconds
(without alignments)
98.565 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQQWNPAGIEAAA 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 11492915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCr_NEM_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	95	9 US-09-805-427A-1	Sequence 1, Appli
2	79	100.0	403	9 US-09-805-427A-4	Sequence 4, Appli
3	79	100.0	403	10 US-09-791-171-173	Sequence 173, App
4	79	100.0	404	9 US-09-805-427A-3	Sequence 3, Appli
5	79	100.0	404	10 US-09-791-171-172	Sequence 172, App
6	59	74.7	20	9 US-10-044-703-60	Sequence 60, Appl
7	59	74.7	20	10 US-09-813-333-59	Sequence 59, Appl
8	43	54.4	13	10 US-09-813-333-59	Sequence 59, Appl
9	43	54.4	13	10 US-09-813-333-59	Sequence 59, Appl
10	43	54.4	20	9 US-10-044-703-61	Sequence 61, Appl
11	43	54.4	20	10 US-09-813-333-61	Sequence 61, Appl
12	40	50.6	295	9 US-09-738-626-4782	Sequence 4782, Ap
13	39	49.4	916	10 US-09-815-242-12006	Sequence 12006, A
14	38	48.1	301	9 US-09-738-626-6880	Sequence 6880, Ap
15	38	48.1	410	10 US-09-847-0818-4	Sequence 4, Appli
16	38	48.1	438	9 US-10-198-070-38	Sequence 38, Appl
17	37	46.8	229	10 US-09-815-242-12391	Sequence 12391, A
18	37	46.8	325	9 US-09-738-626-6035	Sequence 6035, Ap
19	37	46.8	325	9 US-09-746-660A-4	Sequence 4, Appli

20	37	46.8	369	9 US-10-060-218A-6	Sequence 6, Appli
21	37	46.8	463	9 US-10-156-761-12653	Sequence 12653, A
22	37	46.8	739	9 US-10-156-761-10111	Sequence 10111, A
23	36	45.6	221	9 US-10-034-968-155	Sequence 155, App
24	36	45.6	221	10 US-09-739-254-155	Sequence 155, App
25	36	45.6	221	10 US-09-904-615-155	Sequence 35, Appl
26	36	45.6	511	10 US-09-833-745-35	Sequence 54, Appl
27	36	45.6	513	10 US-09-833-745-54	Sequence 1148, A
28	36	45.6	901	10 US-09-815-242-11148	Sequence 7, Appli
29	36	45.6	3070	9 US-09-961-403-7	Sequence 3, Appli
30	35.5	44.9	593	10 US-09-920-021A-3	Sequence 3, Appli
31	35.5	44.9	597	9 US-10-038-010-22	Sequence 22, Appl
32	35	44.3	98	10 US-09-894-018-101	Sequence 101, App
33	35	44.3	153	10 US-09-925-301-1367	Sequence 1367, Ap
34	35	44.3	292	9 US-10-295-403-170	Sequence 170, App
35	35	44.3	301	9 US-10-028-072-176	Sequence 176, App
36	35	44.3	301	9 US-10-121-049-176	Sequence 176, App
37	35	44.3	301	9 US-10-123-904-176	Sequence 176, App
38	35	44.3	301	9 US-10-140-470-176	Sequence 176, App
39	35	44.3	301	9 US-10-175-746-176	Sequence 176, App
40	35	44.3	301	9 US-10-176-918-176	Sequence 176, App
41	35	44.3	301	9 US-10-176-921-176	Sequence 176, App
42	35	44.3	301	9 US-10-137-865-176	Sequence 176, App
43	35	44.3	301	9 US-10-140-474-176	Sequence 176, App
44	35	44.3	301	9 US-10-142-431-176	Sequence 176, App
45	35	44.3	301	9 US-10-143-114-176	Sequence 176, App

ALIGNMENTS

RESULT 1
US-09-805-427A-1
Sequence 1, Application US/09805427A
Patent No. US20020176867A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
FILE REFERENCE: 670001-2002.5
CURRENT APPLICATION NUMBER: US/09/805,427A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 95
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-805-427A-1
Query Match 100.0%; Score 79; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNPAGIEAAA 15
|||||
DB 1 MTEQQWNPAGIEAAA 15

RESULT 2
US-09-805-427A-4
Sequence 4, Application US/09805427A
Patent No. US20020176867A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
FILE REFERENCE: 670001-2002.5
CURRENT APPLICATION NUMBER: US/09/805,427A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 403
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-805-427A-4

Query Match 100.0%; Score 79; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQOMNFAIGIEAAA 15
|||||
DB 22 MTEQOMNFAIGIEAAA 36

RESULT 3
US-09-791-171-173

Sequence 173, Application US/09791171
Patent No. US20020094336A1
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 173
LENGTH: 403
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-791-171-173

Query Match 100.0%; Score 79; DB 10; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQOMNFAIGIEAAA 15
|||||
DB 22 MTEQOMNFAIGIEAAA 36

RESULT 4
US-09-805-427A-3

Sequence 3, Application US/09805427A
Patent No. US20020176867A1
GENERAL INFORMATION:
APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
FILE REFERENCE: 670001-2002.5
CURRENT APPLICATION NUMBER: US/09/805,427A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln version 3.0
SEQ ID NO 3
LENGTH: 404
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-805-427A-3

Query Match 100.0%; Score 79; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQOMNFAIGIEAAA 15
|||||
DB 310 MTEQOMNFAIGIEAAA 324

RESULT 5
US-09-791-171-172

Sequence 172, Application US/09791171
Patent No. US20020094336A1
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 172
LENGTH: 404
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-791-171-172

Query Match 100.0%; Score 79; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEQOMNFAIGIEAAA 15
|||||
DB 310 MTEQOMNFAIGIEAAA 324

RESULT 6
US-10-044-703-60

Sequence 60, Application US/10044703
Publication No. US20020192233A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
CURRENT APPLICATION NUMBER: US/10/044,703
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/190,834
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 60

LENGTH: 20
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-044-703-60

Query Match 74.7%; Score 59; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 OWNFAGIEAAA 15
|||||
DB 1 OWNFAGIEAAA 11

RESULT 7
US-09-813-333-60
Sequence 60, Application US/09813333
Patent No. US20020119160A1
GENERAL INFORMATION:

APPLICANT: Degroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
CURRENT APPLICATION NUMBER: US/09/813,333
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,834
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
LENGTH: 20
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-813-333-60

Query Match 74.7%; Score 59; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 OWNFAGIEAAA 15
|||||
DB 1 OWNFAGIEAAA 11

RESULT 8
US-10-044-703-59
Sequence 59, Application US/10044703
Publication No. US20020192233A1
GENERAL INFORMATION:

APPLICANT: Degroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
CURRENT APPLICATION NUMBER: US/10/044,703
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/190,834
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 13
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-044-703-59

Query Match 54.4%; Score 43; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NFAGIEAAA 15
|||||
DB 1 NFAGIEAAA 9

RESULT 9

US-09-813-333-59
Sequence 59, Application US/09813333
Patent No. US20020119160A1
GENERAL INFORMATION:

APPLICANT: Degroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
CURRENT APPLICATION NUMBER: US/09/813,333
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,834
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 13
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-813-333-59

Query Match 54.4%; Score 43; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NFAGIEAAA 15
|||||
DB 1 NFAGIEAAA 9

RESULT 10
US-10-044-703-61
Sequence 61, Application US/10044703
Publication No. US20020192233A1
GENERAL INFORMATION:

APPLICANT: Degroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
CURRENT APPLICATION NUMBER: US/10/044,703
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/190,834
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 20
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-044-703-61

Query Match 54.4%; Score 43; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NFAGIEAAA 15
|||||
DB 1 NFAGIEAAA 9

RESULT 11
US-09-813-333-61
Sequence 61, Application US/09813333
Patent No. US20020119160A1
GENERAL INFORMATION:

APPLICANT: Degroot, Anne S
TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
FILE REFERENCE: 17999-004 US
CURRENT APPLICATION NUMBER: US/09/813,333
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,834
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 20

;; TYPE: PRT
;; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-61

Query Match
Best Local Similarity 54.4%; Score 43; DB 10; Length 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAAA 15
Db 1 NFAGIEAAA 9

RESULT 12
US-09-738-626-4782
; Sequence 4782, Application US/09738626
; Publication No. US20020197605A1

;; GENERAL INFORMATION:
;; APPLICANT: NAKAGAWA, SATOSHI
;; APPLICANT: MIZOGUCHI, HIROSHI
;; APPLICANT: ANDO, SEIKO
;; APPLICANT: HAYASHI, MIKIRO
;; APPLICANT: OCHIAI, KEIKO
;; APPLICANT: YOKOI, HARUHIKO
;; APPLICANT: TATEISHI, NAOKO
;; APPLICANT: SENOH, AKIHIRO
;; APPLICANT: IKEDA, MASATO
;; APPLICANT: OZAKI, AKIO
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-125
;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 4782
;; LENGTH: 295
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4782

Query Match
Best Local Similarity 50.6%; Score 40; DB 9; Length 295;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOMNFA 9
Db 50 LTEEEMNYA 58

RESULT 13
US-09-815-242-12006
; Sequence 12006, Application US/09815242
; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; CURRENT FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12006
;; LENGTH: 916
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12006

Query Match
Best Local Similarity 49.4%; Score 39; DB 10; Length 916;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOMNFAGIEAA 14
Db 699 EQMDIEGLEAA 709

RESULT 14
US-09-738-626-6880
; Sequence 6880, Application US/09738626
; Publication No. US20020197605A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAGAWA, SATOSHI
;; APPLICANT: MIZOGUCHI, HIROSHI
;; APPLICANT: ANDO, SEIKO
;; APPLICANT: HAYASHI, MIKIRO
;; APPLICANT: OCHIAI, KEIKO
;; APPLICANT: YOKOI, HARUHIKO
;; APPLICANT: TATEISHI, NAOKO
;; APPLICANT: SENOH, AKIHIRO
;; APPLICANT: IKEDA, MASATO
;; APPLICANT: OZAKI, AKIO
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-125
;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 6880
;; LENGTH: 301
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6880

Query Match
Best Local Similarity 48.1%; Score 38; DB 9; Length 301;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTEQOMNFA 9
Db 57 LTEEEMNYA 65

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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:03:09 ; Search time 24 Seconds
(without alignments)
128.779 Million cell updates/sec

Title: US-09-830-839-1
Perfect score: 79
Sequence: 1 MTEQWNPAGIEA 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	54.4	217	16	Q9KMY8
2	43	54.4	247	16	Q8X3F8
3	42	53.2	369	16	Q9Z839
4	42	53.2	723	16	Q9A279
5	41	51.9	182	2	P95622
6	41	51.9	440	2	Q9PAD1
7	41	51.9	443	2	Q9AMK7
8	41	51.9	443	16	Q9KVV6
9	41	51.9	471	17	Q28786
10	41	51.9	934	16	Q8XVJ6
11	40	50.6	38	16	Q9KTC4
12	39	49.4	81	16	Q981F7
13	39	49.4	219	16	Q8YVX4
14	39	49.4	282	2	Q8K0L0
15	39	49.4	325	5	Q966M0
16	39	49.4	328	16	O51337

17	39	49.4	393	16	Q8YTF8	Q8YTF8 anabaena sp
18	39	49.4	482	10	O04629	O04629 arabidopsis
19	39	49.4	598	10	O8W4E7	O8W4E7 arabidopsis
20	39	49.4	714	16	Q9CE55	Q9CE55 lactococcus
21	39	49.4	916	16	Q9LCT3	Q9LCT3 pseudomonas
22	38.5	48.7	372	16	Q98B08	Q98B08 rhizobium 1
23	38.5	48.7	392	16	Q9A560	Q9A560 caulobacter
24	38	48.1	282	2	Q9R6C8	Q9R6C8 agrobacteri
25	38	48.1	284	16	Q9PH66	Q9PH66 xyella fas
26	38	48.1	319	16	Q8UD90	Q8UD90 agrobacteri
27	38	48.1	328	10	Q41401	Q41401 sesbania ro
28	38	48.1	388	2	O52197	O52197 azotobacter
29	38	48.1	393	16	Q9EWU0	Q9EWU0 streptomyce
30	38	48.1	415	16	Q92005	Q92005 rhizobium m
31	38	48.1	443	16	O8ZN34	O8ZN34 salmonella
32	38	48.1	443	16	O8Z4M1	O8Z4M1 salmonella
33	38	48.1	806	3	Q9P4T8	Q9P4T8 agarticus bi
34	38	48.1	885	2	O46002	O46002 clostridium
35	38	48.1	2555	11	Q91ZB5	Q91ZB5 mus musculu
36	38	48.1	2561	11	O8VIE5	O8VIE5 mus musculu
37	37	46.8	61	16	O8X3Q2	O8X3Q2 escherichia
38	37	46.8	108	17	O8TPE1	O8TPE1 methanosarc
39	37	46.8	156	2	Q93D85	Q93D85 streptococc
40	37	46.8	219	5	O95V33	O95V33 spodioplera
41	37	46.8	229	16	Q9S6G3	Q9S6G3 staphylococ
42	37	46.8	251	16	Q9JYE0	Q9JYE0 neisseria m
43	37	46.8	251	16	Q9JME7	Q9JME7 neisseria m
44	37	46.8	253	2	O32816	O32816 lactococcus
45	37	46.8	256	16	O8YA41	O8YA41 listeria mo

ALIGNMENTS

RESULT 1
Q9KMY8 PRELIMINARY; PRT; 217 AA.

AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 21, Last annotation update)
DE F1ne Protein.
GN VCA0178.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L., Dodson R.D., Hatt D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae."
RT Nature 406:477-483(2000).
RL EMBL: AE004358; AAF96091.1; -
DR TIGR: VCA0178; -
DR InterPro: IPR004287; HCCA_isomerase.
DR Pfam: PF03046; HCCA_isomerase; 1.
KW Complete proteome.
SQ SEQUENCE 217 AA; 24897 MW; 79B473E3213B5E8 CRC64;

Query Match 54.4%; Score 43; DB 16; Length 217;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
2 TEOQWNPAGIEA 13
||||| ||| |

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DB      170 TEQGWLAGIHA 181

RESULT 2
ID      08X3F8      PRELIMINARY;      PRT;      247 AA.
AC      08X3F8
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Hypothetical protein Ecs1576.
GN      Ecs1576.
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
OX      NCBI_TaxID=83334;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / RIND 0509952;
RX      MEDLINE=21156231; PubMed=11258796;
RA      Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA      Han C.-G., Ohnabu E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA      Ikeda T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA      Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT      "Complete genome sequence of enterohemorrhagic Escherichia coli
RT      O157:H7 and genomic comparison with a laboratory strain k-12."
RL      DNA Res. 8:11-22(2001).
DR      EMBL: AP002555; BAB34999.1; -.
DR      InterPro: IPR000508: SigPase.
DR      PROSITE: PS00761: SPASE_1_3; UNKNOWN_1.
KW      Hypothetical protein.
SQ      SEQUENCE 247 AA: 27429 MW: 676680113259AB70 CRC64;

Query Match      54.4%; Score 43; DB 16; Length 247;
Best Local Similarity 53.8%; Pred. NO. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0.

OY      3 EQQWAFACIEAAN 15
DB      22 OQMGFSGIKRKA 34
      : 1 1 1 1 1 : 11

RESULT 3
ID      09Z839      PRELIMINARY;      PRT;      369 AA.
AC      09Z839;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      FE-S oxidoreductase.
GN      CPN0513 OR CPJ0513 OR CPJ0240.
OS      Chlamydia pneumoniae (Chlamydia pneumoniae).
OC      Bacteria; Chlamydiales; Chlamydiales; Chlamydia.
OC      NCBI_TaxID=83558;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CTL029;
RX      MEDLINE=99206606; PubMed=10192388;
RA      Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA      Olinger L., Glimm J., Davis R.W., Stephens R.S.;
RT      "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL      Nat. Genet. 21:385-389(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=AR39;
RX      MEDLINE=20150255; PubMed=10684935;
RA      Reed T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA      White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA      Lihner K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA      Gwin M., Nelson W., Deboy R., Kolony J., McClarty G., Salzberg S.L.,
RA      Eisen J., Fraser C.M.;
RT      "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
      pneumoniae AR39."

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RL Nucleic Acids Res. 28:1397-1406(2000).
[3]
SEQUENCE FROM N.A.
RP STRAIN-J138;
RX MEDLINE-20330349; PubMed-10871362;
RA Shiba T., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RT Shiba T., Ishii K., Hattori M., Kubata S., Nakazawa T.;
RL "Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CML029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AE001636; AAD18653.1; -
DR EMBL; AE002184; AAF8105.1; -
DR EMBL; AP002546; BAA98719.1; -
DR TIGR; CP0240; -
DR InterPro; IPR005244; Cons_hypoth423.
DR TIGRFAMs; TIGR00423; TIGR00423.1.
KW Complete proteome.
SQ SEQUENCE 369 AA; 41556 MW; 05AC33C15479B192 CRC64;

Query Match 53.2%; Score 42; DB 16; Length 369;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 WNPAGIEAA 14
DB 305 WNYLGIEAA 313

RESULT 4
O9A279 PRELIMINARY; PRT; 723 AA.
ID O9A279
AC O9A279;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Prolyl oligopeptidase family protein.
GN CC3687.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
CX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE-21173698; PubMed-11259647;
RA Niermen W.C., Feldblyum T.V., Land M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Porocko I., Nelson W.C., Newton A., Stephens C., Placke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwyn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Ueberbeck T., Tran K., Wolf A., Yamathavan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE006026; AAK35649.1; -
DR TIGR; CC3687; -
DR InterPro; IPR001375; Peptidase_S9
DR InterPro; IPR004106; Peptidase_S9_N.
DR InterPro; IPR002470; ProLigo_Prase.
DR InterPro; IPR000379; Ser_estr_site.
DR Pfam; PF00326; Peptidase_S9_1.
DR Pfam; PF02897; Peptidase_S9_N_1.
DR PRINTS; PR00862; PROLIGOPTASE.
KW Complete proteome.
SQ SEQUENCE 723 AA; 78547 MW; 05FB0515D74819A8 CRC64;

Query Match 53.2%; Score 42; DB 16; Length 723;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 TEQOMNPAIGIEAA 15
DB 316 TEQPMNPAIGVIPA 329

```

RESULT 5

Query Match 51.9%; Score 41; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 2 TEQOMNFRAG 10
51 TEEMTFAG 59

AC P95622 PRELIMINARY; PRT; 182 AA.
AC P95622;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Cytochrome c1 (Fragment).
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=384;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97158229; PubMed=9004501;
RA Wu G., Delgado M.J., Vargas C., Davies A.E., Poole R.K., Downie J.A.;
RT "The cytochrome bcl complex but not Cym is necessary for symbiotic
nitrogen fixation by Rhizobium leguminosarum.";
RL Microbiology 142:3381-3388(1996).
DR EMBL: X98018; CA66651.1; -;
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR002326; CytC.
DR Pfam: PF02167; Cytochrome_C1; 1.
DR PRINTS: PR00603; CYTOCHROME_C1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
FT NON TER 182
SQ SEQUENCE 182 AA; 19787 MW; BC1C7255859D44B8 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 2 TEQOMNFRAG 10
51 TEEMTFAG 59

AC P95622 PRELIMINARY; PRT; 440 AA.
AC P95622;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CdB.
GN CdB.
OS Moritella japonica.
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
CC Moritella.
OX NCBI_TaxID=89067;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSK1;
RA Li L., Fujii S., Kato C., Koki H.;
RT "Expression of Lysin Decarboxylase Gene Is Regulated by Pressure in a
RT Deep-Sea Piezophilic Bacterium, Moritella japonica.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB041735; BAB16717.1; -;
DR InterPro: IPR002293; AA/rel_pmeasel.
DR InterPro: IPR004841; Pemease.
DR Pfam: PF00324; aa_permeases; 1.
SQ SEQUENCE 440 AA; 45577 MW; DBD6ACADF8958CD9 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 440;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 6 WNFAGIEAAA 15
199 WSFVGVESAA 208

RESULT 7

Query Match 51.9%; Score 41; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 6 WNFAGIEAAA 15
199 WSFVGVESAA 208

AC P95622 PRELIMINARY; PRT; 443 AA.
AC P95622;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cadaverine/lysine antiporter.
GN CdB.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhee J., Lee J., Lee S., Chung S., Rhee J., Choi S., Ryu P.;
RT "Vibrio vulnificus cadda genes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324470; AAK01663.1; -;
DR InterPro: IPR002293; AA/rel_pmeasel.
DR InterPro: IPR004841; Pemease.
DR Pfam: PF00324; aa_permeases; 1.
SQ SEQUENCE 443 AA; 46752 MW; B88FD7E188036751 CRC64;

Query Match 51.9%; Score 41; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 6 WNFAGIEAAA 15
199 WSFVGVESAA 208

AC P95622 PRELIMINARY; PRT; 445 AA.
AC P95622;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cadaverine/lysine antiporter CdB, putative.
GN VC0280.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EL TOR N16961 / SEROTYPE O1;
RA MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Mierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL: AE004116; AAF93455.1; -;
DR TIGR: VC0280; -;
DR InterPro: IPR002293; AA/rel_pmeasel.
DR InterPro: IPR004841; Pemease.
DR Pfam: PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 445 AA; 46907 MW; 3A64F21B9680684C CRC64;

Query Match 51.9%; Score 41; DB 16; Length 445;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 6 WNFAGIEAAA 15
199 WSFVGVESAA 208

Db 199 MSFVGVESAA 208

RESULT 9

ID 028786 PRELIMINARY; PRT; 471 AA.

AC 028786;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical protein AF1486.

GN AF1486.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RA MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., Hickey E.K., Peterson J.D.,

RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Kyrpides N.C.,

RA Richardson D.L., Kerkvliet A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-

RT reducing archaeon Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997).

DR EMBL: AE001000; AAB89769.1; -

DR TIGR: AF1486; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 471 AA; 54165 MW; 892A03A47FBD4771 CRC64;

QY Query Match 51.9%; Score 41; DB 17; Length 471;

Best Local Similarity 61.5%; Pred. No. 69;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 3 EQQWNPAGIEA 15

08XVJ6

AC 08XVJ6 PRELIMINARY; PRT; 934 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Probable preprotein translocase SECA subunit.

GN SECA OR RSC2834 OR RS00271.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM1100;

RA MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Chardot M., Billault A., Brotlier P., Camus J.C., Catolico L.,

RA Arlet M., Choisme N., Claudel-Renard C., Cunne S., Demange N.,

RA Gaspin C., Lawie M., Moisan A., Robert C., Saurin W., Schlex T.,

RA Siguler P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weisenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).

DR EMBL: AL646072; CAD16541.1; -

DR InterPro: IPR000185; SECA.

DR InterPro: IPR004027; SEC_C_motif.

DR Pfam: PF02810; SEC-C; 1.

DR Pfam: PF01043; SECA_protein; 1.

DR PRINTS: PR00906; SECA.

DR TIGRFAMs: TIGR00963; seca; 1.

DR PROSITE: PS01312; SECA; 1.

KW Complete proteome.

SQ SEQUENCE 934 AA; 105241 MW; F9C3FA601EA62095 CRC64;

QY Query Match 51.9%; Score 41; DB 16; Length 934;

Best Local Similarity 60.0%; Pred. No. 1,4e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 708 EQQWDLGLE 717

09KTC4

AC 09KTC4 PRELIMINARY; PRT; 38 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Hypothetical protein VC0978.

GN VC0978.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N16961 / SEROTYPE O1;

RA MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

RA Emolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio

RT cholerae.";

RL Nature 406:477-483(2000).

DR EMBL: AE004179; AAF94140.1; -

DR TIGR: VC0978; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 38 AA; 4427 MW; 3077749E7004F910 CRC64;

QY Query Match 50.6%; Score 40; DB 16; Length 38;

Best Local Similarity 50.0%; Pred. No. 7.9;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 1 MTEQWNPAGIEA 14

098IF7

AC 098IF7 PRELIMINARY; PRT; 81 AA.

DT 01-OCT-2001 (TREMBLrel. 18, Created)

DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical protein msr2423.

GN MSR2423.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

PS Claim 1; Page 3; 33pp; English.

XX
CC The present sequence is the peptide ES1 derived from the Mycobacterium
CC tuberculosis ESAT-6 gene. This sequence is one of eleven peptides
CC derived from the ESAT-6 gene (see AAY94590 to AAY94600). The peptides
CC are recognised, to varying degrees, by the T cells of patients with
CC tuberculosis. When the peptides are combined together as a panel they
CC provide a high specificity and sensitivity diagnostic test for
CC M. tuberculosis infection. This test has the advantage that it does not
CC give false positives for patients who have been vaccinated with BCG.

XX Sequence 15 AA:

Query Match 100.0%; Score 79; DB 21; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNPAGIEAAA 15

DB 1 MTEOQWNPAGIEAAA 15

RESULT 2

ID AAO17432 standard; peptide; 15 AA.

XX AAO17432;

DT 11-JUL-2002 (first entry)

DE Early secreted antigenic target 6 T cell epitope #1.

XX Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;

KW poxvirus vector; HIV; malaria; Helicobacter pylori; influenza;

KW hepatitis; viral infection; leprosy; protozoan parasite; cancer;

KW tuberculosis; anti-HIV; protozoicide; antibacterial; virucide;

XX hepatotropic; anti-inflammatory; antileptotic; cytostatic; epitope.

OS Mycobacterium tuberculosis.

XX WO200224224-A2.

XX 28-MAR-2002.

XX 13-SEP-2001; 2001WO-GB04116.

XX 21-SEP-2000; 2000GB-0023203.

XX (OXO-) OXON PHARMACINES LTD.

XX H111 AWS, McShane H, Gilbert S, Reece W, Schneider J;

XX WPI; 2002-394098/42.

XX Inducing CD4+ T-cell response against target antigen by administering a

XX composition comprising a source of CD4+ epitopes which is a

XX non-replicating or replication impaired recombinant poxvirus vector

XX Example 1; Page 21; 50pp; English.

XX The present invention relates to a method of inducing a CD4+ T-cell
XX response against a target antigen, by administering two different
XX compositions comprising a source of CD4+ T-cell epitope(s) of the target
XX antigen, where the second composition further includes an epitope which
XX is same as the epitope of the first composition, where the source of the
XX epitopes for the compositions is a non-replicating or replication
XX impaired recombinant poxvirus vector. The methods are useful for inducing
XX CD4+ T-cell immune responses against diseases such as tuberculosis, human
XX immunodeficiency virus (HIV) (persistent viral infection), malaria,
XX Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
XX cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
XX leprosy and diseases caused by non-malarial protozoan parasite such as
XX toxoplasma and cancer. The present sequence is an epitope from

CC Mycobacterium tuberculosis useful in the method of the invention.

XX Sequence 15 AA:

Query Match 100.0%; Score 79; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNPAGIEAAA 15

DB 1 MTEOQWNPAGIEAAA 15

RESULT 3

ID AAY8581 standard; peptide; 17 AA.

XX AAY8581;

DT 11-AUG-2000 (first entry)

DE Antigenic N-terminal sequence of ESAT-6.

XX Ligand presenting assembly; early secreted antigen target 6; ESAT-6;

KW bacteria; detect; diagnosis; allergen; cancer; vaccine; immune response;

KW neurotropic factor; autoimmune-system related compound; IPA; fungi;

XX parasite; cell-adhesion molecule.

OS Mycobacterium tuberculosis.

XX Key

XX Cross-links

XX 17

XX /note- "Ala at position 17 is linked via a linker to Ala

XX at position 17 of an identical peptide, where

XX the linker is COCH2-CH(NH-Lys)-CH2CO, and the

XX Lys residue contained in the linker is also

XX linked to another peptide (see AAY8579)." WO200018791-A1.

XX 06-APR-2000.

XX 29-SEP-1999; 99WO-DK00510.

XX 29-SEP-1998; 98DK-0001233.

XX (STAT-) STATENS SERUM INST.

XX (HOLM/) HOLM A.

XX Holm A, Jorgensen RM, Ostergaard S, Theisen M;

XX WPI; 2000-303438/26.

XX New ligand presenting assemblies useful for diagnosis, treatment and

XX prevention of diseases caused by e.g. viruses, bacteria, toxins,

XX allergens, autoimmune system-related compounds, cancer-related

XX compounds, cell adhesion molecules

XX Claim 34; Page 81; 100pp; English.

XX This sequence represents an antigenic N-terminal sequence from the
XX Mycobacterium tuberculosis early secreted antigenic target 6 (ESAT-6)
XX protein. The peptide is presented on the new ligand presenting assembly
XX of the invention. The invention relates to method for preparing ligand
XX presenting assemblies (LPAs) comprising:
XX (a) providing by solid phase synthesis, or fragment coupling, ligands
XX comprising desired sequences (e.g. the present sequence), the ligands
XX being attached to a solid phase;
XX (b) if necessary, deprotecting any N-terminal amino groups while the
XX ligands are still attached to the solid phase;
XX (c) reacting the ligands having unprotected N-terminal amino groups with
XX an achiral di-, tri- or tetracarboxylic acid, to provide a construct
XX having a ring structure; and

CC (d) cleaving the construct from the solid phase, to provide an LPA
CC comprising ligands having free C-terminal groups. The LPAs can be used
CC for raising an immune response in an animal. They can also be used in
CC vaccines and for generating antibodies in an animal. Alternatively they
CC can be used for the treatment, alleviation, detection, diagnosis, or
CC prophylaxis of diseases caused by viruses, bacteria, toxins, allergens,
CC autoimmune system-related compounds, cancer related compounds, cell
CC adhesion molecules, neurotropic factors, fungi or parasites. Use of the
CC method enables the preparation of very long ring systems interconnected
CC by reaction with the achiral di-, tri- or tetracarboxylic acid. The ring
CC structure formed between desired sequences further enables additional
CC presentation of desired sequences and chemical moieties. The LPAs provide
CC very flexible systems for polyfunctional constructs, and furthermore,
CC products of high purity are obtained.

SO Sequence 17 AA;

Query Match 100.0%; Score 79; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
DB 1 MTEQOWNFAGIEAAA 15

RESULT 4

AAW35548
ID AAW35548 standard; peptide; 19 AA.

AC AAW35548;

DT 22-APR-1998 (first entry)

DE ESAT-6 antigen SEQ ID NO:120 from WO9738011.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
KM scaffold; inhibition; metastasis; wound healing; solid phase.

XX Synthetic.

PN WO9738011-A1.

PD 16-OCT-1997.

PF 03-APR-1997; 97WO-DE00146.

PR 03-APR-1996; 96DK-0000398.

PA (PEPR-) PEPRESEARCH AS.

PI Heegaard PMH, Jakobsen PH;

DR WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a
PT diagnostic agent and as a scaffold for production of chemical
PT derivatives

PS Example 32; Page 156; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence
CC represents a peptide used in an example from the present invention. An
CC (A)-solid phase complex can be used as a scaffold for the production of
CC chemical derivatives, characterised by covalently attaching molecules at
CC attachment points. Alternatively (A) is used as a scaffold-peptide for
CC the incorporation into an immunostimulating complex (iscom) resulting an
CC (A)-iscom complex which is used for the chemical coupling of antigenic

CC substances in an aqueous solution by conjugation. (A) derivatised with
CC one or more peptides having fibronectin-, laminin- or vitronectin-like
CC binding activities can be used for the promotion of cell-attachment to
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
CC and for promotion of wound healing. Also a derivatised (A) can be used
CC for the selection of specifically-binding aptamers or as a diagnostic
CC agent. Such diagnostic-(A) molecules could be used to detect molecules
CC derived from or indicative of pregnancy or of a disease, such as an
CC infectious, autoimmune or cancerous disease.

SO Sequence 19 AA;

Query Match 100.0%; Score 79; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAA 15
DB 1 MTEQOWNFAGIEAAA 15

RESULT 5

AAW32466
ID AAW32466 standard; Protein; 51 AA.

AC AAW32466;

DT 09-JAN-1998 (first entry)

DE Mycobacterium tuberculosis antigen ESAT-6.

XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;

KM skin testing; M.tuberculosis.

OS Mycobacterium tuberculosis.

PN WO9709428-A2.

PD 13-MAR-1997.

PF 30-AUG-1996; 96WO-US14674.

PR 12-JUL-1996; 96US-0680574.

PR 01-SEP-1995; 95US-0523436.

PR 22-SEP-1995; 95US-0533634.

PR 22-MAR-1996; 96US-0620874.

PR 05-JUN-1996; 96US-0659683.

PA (CORI-) CORIXA CORP.

PI Campos-melo A, Dillon DC, Houghton R, Reed SG, Skelky YAW;

PI Twardzik DR, Vedvick TH;

DR N-PSDB; AAT91529.

DR WPI; 1997-192903/17.

XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
PT useful in vaccines for prevention or treatment of tuberculosis, also
PT for diagnosis

PS Disclosure; Page 135; 168pp; English.

CC A new immunogenic polypeptide has been developed comprising an
CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or
CC its variant differing only in conservative substitutions and/or
CC modifications). The present sequence represents a M.tuberculosis
CC antigen, ESAT-6. The immunogenic protein, and fusion proteins
CC containing one or more of the proteins or one of the proteins plus a
CC ESAT-6, are useful in vaccines, preferably when formulated with a
CC non-specific adjuvant, to induce an immune response against
CC M.tuberculosis (for treatment or prevention).

Query Match 100.0%; Score 79; DB 18; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNFAGIEAAA 15
 |||||
 DB 1 MTEOQWNFAGIEAAA 15

RESULT 6

AAW32339
 ID AAW32339 standard; Protein; 51 AA.

AC AAW32339;

XX 13-JAN-1998 (first entry)

DE Mycobacterium tuberculosis antigen ESAT-6.

KW Antigen; Immunogen; vaccine; tuberculosis; non specific adjuvant;
 KM skin testing; M.tuberculosis.

XX Mycobacterium tuberculosis.

PN WO9709429-A2.

PD 13-MAR-1997.

PF 30-AUG-1996; 96WO-US14675.

PR 12-JUL-1996; 96US-0680573.

PR 01-SEP-1995; 95US-0523435.

PR 22-SEP-1995; 95US-0532136.

PR 22-MAR-1996; 96US-0620280.

PR 05-JUN-1996; 96US-0658800.

XX (CORI-) CORIXA CORP.

PI Campos-neto A, Dillon DC, Houghton R, Reed SG, Skelky YAW,
 Twardzik DR, Vedvick TH;

XX WPI: 1997-192904/17.

DR N-PSDB: AAT91463.

XX New immunogenic polypeptide(s) from soluble M. tuberculosis antigens
 PT - useful for diagnosis of M. tuberculosis infection

XX Claim 43; Page 147; 190pp; English.

XX A new immunogenic polypeptide has been developed comprising an
 CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or
 CC its variant differing only in conservative substitutions and/or
 CC modifications). The present sequence represents a specifically claimed
 CC sequence of the ESAT-6 M.tuberculosis antigen. The immunogenic
 CC polypeptide can be used to diagnose M.tuberculosis infection by forming
 CC complexes with specific antibodies in the sample. Fragments of DNA
 CC encoding the immunogenic polypeptide can be used as diagnostic primers
 CC or probes and agents that bind to the antigen, especially monoclonal
 CC antibodies or equivalent polyclonal antibodies, are also used for
 CC diagnosis.

XX Sequence 51 AA;

SO Query Match 100.0%; Score 79; DB 18; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNFAGIEAAA 15
 |||||
 DB 1 MTEOQWNFAGIEAAA 15

RESULT 7
 AAW81701
 ID AAW81701 standard; Protein; 51 AA.

XX AAW81701;

XX 27-JAN-1999 (first entry)

DE M. tuberculosis immunogenic polypeptide ESAT-6.

KW Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
 KM vaccine; pharmaceutical; infection; diagnosis.

XX Mycobacterium tuberculosis.

PN WO9816646-A2.

PD 23-APR-1998.

PF 07-OCT-1997; 97WO-US18293.

PR 13-MAR-1997; 97US-0818112.

PR 11-OCT-1996; 96US-0730510.

XX (CORI-) CORIXA CORP.

PI Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
 Reed SG, Skelky YAW, Twardzik DR, Vedvick TS;

XX WPI: 1998-261042/23.

XX N-PSDB: AAW64501.

XX Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used
 PT to develop products for the detection of M. tuberculosis infection
 PT and for diagnosis, treatment and prevention of tuberculosis

XX Disclosure; Page 126; 230pp; English.

XX This sequence represents an immunogenic portion of a soluble
 CC Mycobacterium tuberculosis (MT) antigen which can be used in a method
 CC for inducing protective immunity against tuberculosis (TB). This
 CC sequence can be formulated into vaccines and/or pharmaceutical
 CC compositions for immunising against M. tuberculosis infection or may
 CC be used for the diagnosis of tuberculosis.

XX Sequence 51 AA;

SO Query Match 100.0%; Score 79; DB 19; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNFAGIEAAA 15
 |||||
 DB 1 MTEOQWNFAGIEAAA 15

RESULT 8

AAW64334
 ID AAW64334 standard; Protein; 51 AA.

XX AAW64334;

XX 09-NOV-1998 (first entry)

DE Mycobacterium tuberculosis antigen ESAT-6.

KW Tuberculosis; infection; diagnosis; antigen; ESAT-6.

XX Mycobacterium tuberculosis.

OS WO9816645-A2.

PN 23-APR-1998.

XX 07-OCT-1997; 97WO-US18214.
 PF 13-MAR-1997; 97US-0818111.
 PR 11-OCT-1996; 96US-0729622.
 XX
 PA (CORI-) CORIXA CORP.
 PI Campos-Neto A, Dillon DC, Houghton R, Lodes MJ;
 PI Reed SG, Skeiky YAM, Twardzik DR, Vedvick TS;
 XX
 DR WPI, 1998-251292/22.
 DR N-PSDB; AA44393.
 XX
 PT New isolated Mycobacterium tuberculosis polypeptides and DNA - used
 PT to develop products for the detection of M. tuberculosis infection
 PT and diagnosis of tuberculosis
 PS
 XX Disclosure; Page 130; 250pp; English.
 XX
 CC This polypeptide comprises an antigenic portion of Mycobacterium
 CC tuberculosis antigen ESAT-6. The invention relates to
 CC compositions and methods for diagnosing tuberculosis. It provides
 CC polypeptides (see AA64291-W64379) comprising an antigenic portion
 CC of a soluble M. tuberculosis antigen, or an immunogenic portion of
 CC an M. tuberculosis antigen, as well as fusion proteins between
 CC these polypeptides and known antigens such as ESAT-6. Also claimed
 CC are methods and diagnostic kits for detecting M. tuberculosis
 CC infection in a patient using these polypeptides, antibodies, or
 CC oligonucleotide probes and primers.
 XX
 SQ Sequence 51 AA;

Query Match 100.0%; Score 79; DB 19; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQMNFGIEPAA 15
 ||||||||||||
 1 MTEOQMNFGIEPAA 15
 DB

RESULT 9
 AAY39131
 ID AAY39131 standard; Protein; 51 AA.
 XX
 AC AAY39131;
 XX
 DT 05-NOV-1999 (first entry)
 XX
 DE M. tuberculosis ESAT-6 amino acid sequence.
 XX
 KW Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
 KW immunotherapy; diagnosis; immunisation; vaccine; infection;
 KW immune response; skin test.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9942076-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03268.
 XX
 PR 05-MAY-1998; 98US-0072967.
 PR 18-FEB-1998; 98US-0025197.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAM, Twardzik DR, Vedvick TS;
 XX
 DR WPI, 1999-527409/44.

DR N-PSDB; AA219303.
 XX
 PT New antigens from Mycobacterium tuberculosis useful in diagnostic
 PT skin tests and protective or therapeutic vaccines or compositions
 XX
 PS Disclosure; Page 120; 299pp; English.
 XX
 CC The present invention describes polypeptides comprising an immunogenic
 CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
 CC are vaccines and fusion protein containing M. tuberculosis Ag's.
 CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
 CC other polypeptides fragments, can be used in pharmaceutical compositions
 CC or vaccines to generate a protective or therapeutic immune response to
 CC M. tuberculosis and as reagents in skin tests for diagnosis of
 CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
 CC by, T, B or natural killer cells and/or macrophages in
 CC tuberculosis-immune subjects. AA219249 to AA219460 and AAY39083 to
 CC AAY39225 are used in the exemplification of the present invention.
 XX
 SQ Sequence 51 AA;

Query Match 100.0%; Score 79; DB 20; Length 51;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQMNFGIEPAA 15
 ||||||||||||
 1 MTEOQMNFGIEPAA 15
 DB

RESULT 10
 AAY38988
 ID AAY38988 standard; Protein; 51 AA.
 XX
 AC AAY38988;
 XX
 DT 05-NOV-1999 (first entry)
 XX
 DE M. tuberculosis recombinant antigen protein ESAT-6.
 XX
 KW Antigen; diagnosis; detection; infection; antibody; immunisation;
 KW vaccine; immunity.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9942118-A2.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03265.
 XX
 PR 05-MAY-1998; 98US-0072596.
 PR 18-FEB-1998; 98US-0024753.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAM, Twardzik DR, Vedvick TS;
 XX
 DR WPI, 1999-527416/44.
 DR N-PSDB; AA219091.
 XX
 PT New polypeptide comprising antigenic portions of M. tuberculosis
 XX
 PS Claim 51; Page 165; 323pp; English.
 XX
 CC This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against
 CC M. tuberculosis infection. The new detection methods are needed as
 CC current vaccination strategies do not provide 100% immunity.

[illegible][illegible]

DE ESAT6.
XX
KM ESAT6: Mycobacterium tuberculosis: 6kDa antigen; tuberculosis complex;
KM HYB76-8 reactive antigen; interferon-gamma; memory T-lymphocyte; vaccine;
KM M. africanum; M. bovis; delayed-type hypersensitivity reaction; therapy.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9501441-A1.
XX
PD 12-JAN-1995.
XX
PF 01-JUL-1994; 94MO-DK00273.
XX
PR 02-JUL-1993; 93DK-0000798.
XX
PA (STAT-) STATENS SERUMINSTITUTT.
XX
PI Andersen AB, Andersen P, Haslov K, Sorensen A;
XX
DR WPI: 1995-061005/08.
DR N-PSDB: AAT51422.
XX
XX Vaccine for tuberculosis induces interferon-gamma release from
PT T-lymphocytes - comprises an antigen released from mycobacteria,
PT for immunisation of humans
XX
PS Claim 5; Page 61-63; 101pp; English.
XX
CC This sequence represents the Mycobacterium tuberculosis ESAT6. ESAT6 is
CC also known as the 6kDa antigen, or the HYB76-8 reactive antigen. ESAT6
CC is released from metabolising bacteria, and can be isolated from short
CC term filtrates grown as shaken cultures for 7 days. ESAT6 also induces a
CC release of interferon-gamma from reactivated memory T-lymphocytes. This
CC protein sequence is included in the vaccine of the invention. The
CC vaccine is for immunising an animal (including humans) against
CC tuberculosis caused by a Mycobacterium belonging to the tuberculosis
CC complex. The Mycobacterium of the tuberculosis complex are, M.
CC tuberculosis, M. africanum, and M. bovis. The vaccine can evoke a
CC protective immune response against tuberculosis or a delayed-type
CC hypersensitivity reaction. The protein can also be included in a
CC composition for diagnosing tuberculosis. The composition is injected
CC intradermally, and a skin reaction is an indicator of tuberculosis.
CC
XX
SQ Sequence 95 AA;
Query Match 100.0%; Score 79; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. NO. 8.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEOQWNPAGIEAANA 15
DB 1 MTEOQWNPAGIEAANA 15
RESULT 14
AAY29890
ID AAY29890 standard; Protein: 95 AA.
XX
AC AAY29890;
XX
DT 18-NOV-1999 (first entry)
XX
DE Mycobacterium tuberculosis ESAT-6 protein sequence.
XX
KM Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
KM delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
KM interferon-gamma release.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9945119-A2.
XX
PD

PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99MO-DK00109.
XX
PR 06-MAR-1998; 98DK-0000306.
PR 06-MAR-1998; 98US-0077105.
XX
PA (STAT-) STATENS SERUM INST.
XX
PI Jensen CL, Folkersen J;
XX
DR WPI: 1999-551043/46.
DR N-PSDB: AAZ21132.
XX
XX New mycobacterial polypeptide produced in lactic acid bacteria, useful
PT in tuberculosis diagnosis and vaccines
XX
PS Disclosure; Page 75-76; 76pp; English.
XX
CC The present invention describes a bioactive polypeptide (or
CC immunologically equivalent analogue) produced in lactic acid bacteria
CC which reacts with lymphoid cells primed with Mycobacterium tuberculosis
CC complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The
CC polypeptide and ESAT-6 polypeptides are useful in compositions for
CC diagnosis of and vaccination against tuberculosis caused by
CC M. tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used
CC to diagnose ongoing/previous sensitisation with these bacteria by
CC detecting cytokine release when contacting blood samples with the
CC polypeptide. The bioactive polypeptide may be used in diagnostic
CC compositions and vaccines for mycobacteria other than of the
CC M. tuberculosis complex, e.g. M. avium which infects poultry and
CC occasionally humans, M. leprae; they are especially useful when they do
CC not react with lymphoid cells previously primed with M. tuberculosis
CC complex mycobacteria, and so do not give rise to a diagnostic reaction
CC in individuals infected with these bacteria. The polypeptides may also
CC be used in in vitro diagnostic tests e.g. stimulation of interferon-gamma
CC release from lymphocytes. The polypeptide has similar or higher
CC bioactivity as currently used tuberculin reagent in the standard
CC delayed type hypersensitivity (DTH) skin test for tuberculosis, but may
CC have greater specificity, being better able to discriminate between
CC lymphoid cells primed from tuberculosis and from previous vaccination.
CC The present sequence represents M. tuberculosis ESAT-6 used in the
CC exemplification of the present invention.
CC
XX
SQ Sequence 95 AA;
Query Match 100.0%; Score 79; DB 20; Length 95;
Best Local Similarity 100.0%; Pred. NO. 8.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEOQWNPAGIEAANA 15
DB 1 MTEOQWNPAGIEAANA 15
RESULT 15
AAY29788
ID AAY29788 standard; Protein: 95 AA.
XX
AC AAY29788;
XX
DT 08-NOV-1999 (first entry)
XX
DE Mycobacterial tuberculosis ESAT-6 protein.
XX
KM Mycobacterial; ESAT-6; 6 kDa antigen; tuberculosis; infection;
KM immunological response; diagnosis; vaccine.
XX
OS Mycobacterium tuberculosis.
XX
PN US5955077-A.
XX
PD 21-SEP-1999.

```

XX 05-JUN-1995: 95US-0465640.
PF
XX
PR 05-JUN-1995: 95US-0465640.
PR 20-SEP-1993: 93US-0123182.
PR 01-JUL-1994: 94WO-DK00273.
XX
PA (STAT-) STATENS SERUMINSTITUT.
XX
PI Andersen AB, Andersen P, Haslov K, Sorensen AL;
XX
DR WPI, 1999-539545/45.
DR N-PSDB: AA208877.
XX
PT Polypeptide secreted from Mycobacterium is useful as a vaccine
XX against tuberculosis
XX
PS Claim 24: Fig 10C; 39pp: English.
XX
CC The present invention describes a purified or non-naturally occurring
CC polypeptide (I) released from a metabolising mycobacteria comprising an
CC ESAT6, also called the 6 kDa antigen. The present sequence represents
CC Mycobacterium tuberculosis ESAT-6 protein. Also described is a purified
CC or non-naturally occurring polypeptide (II) with the ability to elicit
CC a delayed type hypersensitivity reaction which comprises a T cell
CC epitope of (I). (II) can be used with a carrier or vehicle in a
CC composition for diagnosing tuberculosis caused by mycobacteria belonging
CC to the tuberculosis complex, i.e. Mycobacterium tuberculosis, M. bovis
CC and M. africanum. The composition can be used to detect microbial
CC antibodies or components of mycobacteria in samples or in animals
CC through the use of immunoassays. (II) can be used as a vaccine for
CC immunising an animal, including humans against tuberculosis caused by
CC mycobacteria of the tuberculosis-complex. (II) induce a release of
CC IFN-gamma from reactivated T-lymphocytes evoking a protective immune
CC response. Vaccine containing (II) has the same protective potency as
CC the live BCG vaccine against tuberculosis.
XX
SQ Sequence 95 AA:

```

```

Query Match 100.0%; Score 79; DB 20; Length 95;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTEQQWNFAGIEAA 15
   |||
Db 1 MTEQQWNFAGIEAA 15

```

Search completed: July 3, 2003, 14:05:31
Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:02:14 ; Search time 6.5 Seconds

(without alignments)
95.715 Million cell updates/sec

Title: US-09-830-839-1

Sequence: 1 MTEGQWNFAGIEAA 15

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	74	93.7	94	1	ESAB_MYCTU	Q57165 mycobacteri
2	45	57.0	476	1	NOEA_RHIME	Q52892 rhizobium m
3	42	53.2	539	1	G6PI_CAUCR	Q9abk5 caulobacter
4	41	51.9	176	1	DSBB_ECOLI	P30018 escherichia
5	41	51.9	176	1	DSBB_SHIFL	Q54155 shigella fl
6	38	48.1	305	1	YNA5_DEIRA	Q93757 deinococcus
7	38	48.1	438	1	SGCE_HUMAN	Q43556 homo sapien
8	38	48.1	444	1	CADB_ECOLI	P23891 escherichia
9	38	48.1	508	1	HMCW_PIG	O02734 sus scrofa
10	38	48.1	2564	1	DREB_CHICK	P18302 gallus gall
11	38	48.1	211	1	MT04_SYNT3	Q9b254 homo sapien
12	37	46.8	264	1	COMT_RAT	P73161 synecocyst
13	37	46.8	294	1	G3P_ESCBL	P22734 rattus norv
14	37	46.8	335	1	YD59_SCHHO	P27749 escherichia
15	37	46.8	354	1	WN11_BRARE	Q10312 schizosacch
16	37	46.8	445	1	YJDE_ECOLI	O73864 brachydanio
17	37	46.8	475	1	GUNA_CLOCE	P17901 clostridium
18	37	46.8	668	1	YMI8_YEAST	Q04511 saccharomyc
19	37	46.8	879	1	STYL_XYLPA	Q9pb98 xyliella fas
20	37	46.8	947	1	LKTA_PASBP	P55123 pasteurella
21	36.5	46.2	131	1	IMBN_SHIDY	P03832 shigella dy
22	36	45.6	148	1	HPCR_ECOLI	O07095 escherichia
23	36	45.6	175	1	RP18_RAT	P47940 rattus norv
24	36	45.6	230	1	TERM_BPCP1	Q37988 bacteriopho
25	36	45.6	326	1	ODPB_RICPR	Q92d13 rickettsia
26	36	45.6	430	1	YPRC_LACPL	P77884 lactobacilli
27	36	45.6	475	1	ARCD_LACSP	O53092 lactobacilli
28	36	45.6	496	1	SRM_MOUSE	O62270 mus musculu
29	36	45.6	499	1	MYRE_BRUME	O84171 bruceella me
30	36	45.6	511	1	HOTH_RHIME	O31197 rhizobium m
31	36	45.6	700	1	FEFG_RALSTO	O84171 bruceella me
32	36	45.6	901	1	SECA_HAEIN	P43803 haemophilus
33	36	45.6	901	1	SECA_HAEIN	P43803 haemophilus

34	36	45.6	964	1	AMPN_RAT	P15684 rattus norv
35	36	45.6	965	1	AMPN_MOUSE	P97449 mus musculu
36	36	45.6	994	1	POLN_MIDTV	P03318 midselburg
37	36	45.6	3106	1	LMW2_MOUSE	O60675 mus musculu
38	36	45.6	3110	1	LMW2_HUMAN	P24043 homo sapien
39	35.5	44.9	585	1	PTNB_MOUSE	P35235 mus musculu
40	35.5	44.9	593	1	PTNB_HUMAN	O06124 homo sapien
41	35.5	44.9	593	1	PTNB_HUMAN	P41498 rattus norv
42	35	44.3	74	1	CKSL_DROME	Q24152 dirosophila
43	35	44.3	82	1	Y4KO_RHISN	P55533 rhizobium s
44	35	44.3	145	1	Y008_MYCTU	P71577 mycobacteri
45	35	44.3	175	1	RP18_MOUSE	P47939 mus musculu

ALIGNMENTS

RESULT 1

ID ESAB_MYCTU STANDARD: PRT: 94 AA.
AC Q57165; 084901;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 6 kDa early secretory antigenic target (ESAT-6).
GN ESAT6 OR RV3875 OR MT3989 OR MTV027.10.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NX NCBI_TaxID=1773, 1765;

[1]
SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=95204931; PubMed=7897219;

RA Andersen P., Andersen A.B., Sorensen A.L., Nagai S.;
RT "Recall of long-lived immunity to Mycobacterium tuberculosis infection
in mice";
RL J. Immunol. 154:3359-3372(1995).

[2]
SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
RX MEDLINE=95247251; PubMed=7729876;
RA Sorensen A.L., Nagai S., Houen G., Anderson P., Anderson A.B.;
RT "Purification and characterization of a low-molecular-mass T-cell
antigen secreted by Mycobacterium tuberculosis";
RL Infect. Immun. 63:1710-1717(1995).

[3]
SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
BA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
RA Hovnsky T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rulston S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence";
RL Nature 393:537-544(1998).

[4]
SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Feldman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains";
RL submitted (APR-2001) to the EMBL/Genbank/DBJ databases.

```

RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis;
RA Singh B., Siddiqui Z., Singh S., Sharma P.;
RT "ESAT-6 gene of a clinical isolate of Mycobacterium tuberculosis from
  India."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis;
RA Mahalingam G.G., Sabo P.J., Hickey M.J., Singh D.C., Storer C.K.;
RT "Molecular analysis of genetic differences between Mycobacterium bovis
  BCG and virulent M. bovis."
RL J. Bacteriol. 178:1274-1282(1996).
RN [7]
RP SEQUENCE OF 1-70 FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RA MEDLINE=96061212; PubMed=9846755;
RX Berthet F., X., Rasmussen P.B., Rosenkrands I., Andersen P.,
  Gicquel B.;
RT "A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel
  low-molecular-mass culture filtrate protein (CFP-10).";
RL Microbiology 144:3195-3203(1998).
CC -1- FUNCTION: NOT KNOWN. ELICITS HIGH LEVEL OF INF-GAMMA FROM MEMORY
  EFFECTOR CELLS DURING THE FIRST PHASE OF A PROTECTIVE IMMUNE
  RESPONSE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
CC -----
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CC -----
CC EMBL: U34848; AAC44033.1; -
CC EMBL: X79562; CA56099.1; -
CC EMBL: AL022120; CA17967.1; -
CC EMBL: AF420491; AAL16896.1; -
CC EMBL: AE007190; AAK48357.1; -
CC EMBL: AF004671; AAC83446.1; -
CC TIGR: MT3989; -
CC TubercuList: RV3875; -
CC Antigen: Complete proteome.
CC INIT_MET 0
CC FT 0
CC SEQUENCE 94 AA; 9773 MW; 19245B0EC478BC84 CRC64;

Query Match 93.7%; Score 74; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TEOQWNFAGIEAAA 15
DB 1 TEOQWNFAGIEAAA 14

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / SU47;
RX MEDLINE=96111489; PubMed=8801423;
RA Ardourel M., Lortet G., Mallet F., Roche P., Truchet G.,
  Promé J.-C., Rosendberg C.;
RT "In Rhizobium meliloti, the operon associated with the nod box n5
  comprises nodJ, noeA and noeB, three host-range genes specifically
  required for the nodulation of particular Medicago species."
RL Mol. Microbiol. 17:687-699(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
  Barloy-Hubler F., Bowser L., Capela D., Galbert F., Gouzy J.,
  Gurjal M., Hong A., Huzar L., Hyman R.W., Kahn M.L.,
  Kalmán S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
  Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
  Sinorhizobium meliloti pSyma megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC -1- FUNCTION: NOT KNOWN. DOES NOT SEEM TO PARTICIPATE IN NOD FACTOR
  SYNTHESIS BUT REQUIRED FOR NODULATION ON SOME SPECIFIC MEDICAGO
  SPECIES SUCH AS M.LITTORALIS.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U26430; AAC44091.1; -
CC EMBL: AE007232; AAK65074.1; -
CC InterPro: IPR000051; SAM_bind.
CC Plasmid: Nodulation; Complete proteome.
CC SEQ 476 AA; 53673 MW; EFOA4009B5F4965E CRC64;

Query Match 57.0%; Score 45; DB 1; Length 476;
Best Local Similarity 63.6%; Pred. No. 2.6;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 5 QWNFAGIEAAA 15
DB 100 QWNFAGIEAAA 110

```

```

RESULT 2
NOEA_RHIME
ID NOEA_RHIME STANDARD; PRT; 476 AA.
AC Q52892;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nodulation protein noeA.
GN NOEA OR RA0416 OR SMA0773.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSyma (megaplasmid 1).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;

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RESULT 3
G6PI_CAUCR
ID G6PI_CAUCR STANDARD; PRT; 539 AA.
AC Q9ABK5;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
  isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR CC0222.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
  Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
  Potocka I., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
  Debay R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
  Kolonay J.F., Smit J., Craven M.B., Kouri H., Shetty J., Berry K.,
  Ullrich T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

```

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate -> D-fructose 6-phosphate.
 CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.

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 DR EMBL; AE005696; AAK22209.1; -
 DR HSSP; Q9N1E2; 1HOX.
 DR TIGR; CC0222; -
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam; PF00342; PGI.1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P-GLUCOSE-ISOMERASE.1; 1.
 DR PROSITE; PS00174; P-GLUCOSE-ISOMERASE.2; 1.
 KM Isomerase: Gluconeogenesis; Glycolysis; Complete proteome.
 FT ACT_SITE 380 380 By SIMILARITY.
 FT ACT_SITE 508 508 By SIMILARITY.
 SQ SEQUENCE 539 AA; 57526 MW; B233DFBAF7FD1595 CRC64;

 Query Match 53.2%; Score 42; DB 1; Length 539;
 Best Local Similarity 50.0%; Pred. No. 9.6;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

 QY 1 MTEQONFACIEAA 14
 Db 48 LSKQWMDGICIEAA 61

 RESULT 4
 ID DSB_ECOLI STANDARD; PRT; 176 AA.
 AC P30018;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Disulfide bond formation protein B (Disulfide oxidoreductase).
 GN DSB OR ROXB OR BIL85 OR Z1948 OR ECS1680.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_Taxid=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=93157338; PubMed=8430071;
 RA Bardwell J.C.A., Lee J.-O., Jander G., Martin N., Belin D.,
 RA Beckwith J.;
 RT "A pathway for disulfide bond formation in vivo."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1038-1042(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93348217; PubMed=7688471;
 RA Masiakos D., Georgopoulos C., Raina S.;
 RT "Identification and characterization of the *Escherichia coli* gene
 RT ddbB, whose product is involved in the formation of disulfide bonds
 RT in vivo."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7084-7088(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-K12 / MG1655;
 RX MEDLINE=9746617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.;
 RT "A 7.8-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533(2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsuki E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 1-169 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=92283803; PubMed=1317851;
 RA Plimer E., Padan E., Schindler S.;
 RT "Cloning, sequencing, and expression of the *nhaB* gene, encoding a
 RT Na⁺/H⁺ antiporter in *Escherichia coli*.";
 RL J. Biol. Chem. 267:11064-11068(1992).
 RN [8]
 RP TOPOLOGY AND MUTAGENESIS OF CYSTEINE RESIDUES.
 RX MEDLINE=95045404; PubMed=7957076;
 RA Jander G., Martin N.L., Beckwith J.;
 RT "Two cysteines in each periplasmic domain of the membrane protein
 RT DsbB are required for its function in protein disulfide bond
 RT formation.";
 RL EMBO J. 13:5121-5127(1994).
 RN [9]
 RP ACTIVE SITES.
 RX MEDLINE=99164086; PubMed=11064586;
 RA Kobayashi T., Ito K.;
 RT "Respiratory chain strongly oxidizes the CXXC motif of DsbB in the
 RT *Escherichia coli* disulfide bond formation pathway.";
 RL EMBO J. 18:1192-1198(1999).
 CC -1- FUNCTION: REQUIRED FOR DISULFIDE BOND FORMATION IN SOME
 CC PERIPLASMIC PROTEINS SUCH AS PHO A OR OMP A. ACTS BY OXIDIZING
 CC THE DSB A PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE DSB FAMILY.

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DR EMBL: L03721; AAA23711.1; ALT_INIT.
 DR EMBL: AE000216; AAC74269.1; -
 DR EMBL: D90752; BAA36032.1; ALT_INIT.
 DR EMBL: D90753; BAA36040.1; ALT_INIT.
 DR EMBL: AE005335; AAG56036.1; -
 DR EMBL: AP002555; BAB35103.1; -
 DR EMBL: M83655; -; NOT_ANNOTATED_CDS.
 DR PIR: JCI109; JCI109.
 DR Ecocore: EG11393; dsdb.
 DR InterPro: IPR003752; Dsdb.
 DR Pfam: PF02600; Dsdb; 1.
 DR Oxidoreductase; Redox-active center; Electron transport; Chaperone;
 KM Oxidoreductase; Inner membrane; Complete proteome;
 FT TRANSMEM 1 14
 FT DOMAIN 1 14
 FT TRANSMEM 15 31
 FT DOMAIN 32 49
 FT TRANSMEM 50 65
 FT DOMAIN 66 71
 FT TRANSMEM 72 89
 FT DOMAIN 90 144
 FT TRANSMEM 145 163
 FT DOMAIN 164 176
 FT DISULFID 41 44
 FT DISULFID 104 130
 FT CONFLICT 50 51
 FT CONFLICT 136 136
 SQ SEQUENCE 176 AA; 2014 MW; 9C8D673D51E9F09B CRC64;

Query Match
 Best Local Similarity 51.9%; Score 41; DB 1; Length 176;
 Matches 6; Conservative 60.0%; Pred. No. 4.7;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 ECOMNFAGIE 12
 1:1:1:1:1:1

DB 132 EROMDFLGIE 141

RESULT 5
 DSB, SHIFL STANDARD; PRT; 176 AA.
 ID Q54155;
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Disulfide bond formation protein B (Disulfide oxidoreductase).
 GN DSB.
 OS *Shigella flexneri*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC *Shigella*.
 NC NCBL_TaxID-623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-YSH6000 / Serotype 2a;
 RA Sasakawa C.;
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBD databases.
 CC -1- FUNCTION: REQUIRED FOR DISULFIDE BOND FORMATION IN SOME
 CC PERIPLASMIC PROTEINS SUCH AS PHO A OR OMPA. ACTS BY OXIDIZING
 CC THE DSB PROTEIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE DSB FAMILY.
 CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: D38254; BAA07408.1; -
 DR InterPro: IPR003752; Dsdb.
 DR Pfam: PF02600; Dsdb; 1.
 DR Oxidoreductase; Redox-active center; Electron transport; Chaperone;
 KM Oxidoreductase; Inner membrane;
 FT TRANSMEM 1 14
 FT DOMAIN 1 14
 FT TRANSMEM 15 31
 FT DOMAIN 32 49
 FT TRANSMEM 50 65
 FT DOMAIN 66 71
 FT TRANSMEM 72 89
 FT DOMAIN 90 144
 FT TRANSMEM 145 162
 FT TRANSMEM 163 176
 FT DISULFID 41 44
 FT DISULFID 104 130
 SQ SEQUENCE 176 AA; 2003 MW; 7532F2B916B72246 CRC64;

Query Match
 Best Local Similarity 51.9%; Score 41; DB 1; Length 176;
 Matches 6; Conservative 60.0%; Pred. No. 4.7;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 ECOMNFAGIE 12
 1:1:1:1:1:1

DB 132 EROMDFLGIE 141

RESULT 6
 YN45_DEIRA STANDARD; PRT; 305 AA.
 ID YN45_DEIRA
 AC Q9RRY7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein DR2345.
 GN DR2345.
 OS *Deinococcus radiodurans*.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 CC Deinococcaceae; Deinococcus.
 NC NCBL_TaxID-1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RX MEDLINE-20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Uyang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RA "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 CC -1- SIMILARITY: BELONGS TO THE UPF0151 FAMILY. SOME SIMILARITY TO
 CC PHOSPHATASES.
 CC -----
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DR EMBL: AE002065; AAF11890.1; -
 DR TIGR: DR2345; -
 DR InterPro: IPR004843; M-peptidase.
 DR InterPro: IPR004844; S/T-phosphatase.
 DR Pfam: PF00149; Metallophos; 1
 KW Hypothetical protein; Hydrolase; Complete proteome.

SQL SEQUENCE 305 AA; 32238 MW; FBF59ADE18CA0F88 CRC64;
Query Match 48.1%; Score 38; DB 1; Length 305;
Best Local Similarity 45.5%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 MTEQOWNFAGI 11
1:1111:
47 VTHEQOWNLVGL 57
DB
RESULT 7
SCCE_HUMAN STANDARD: PRT; 438 AA.
AC 043556;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Epsilon-sarcoglycan precursor (Epsilon-Sg).
GN SCGE OR ESG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Nigro V.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA McNally E.M., Ly C.T., Kunkel L.M.;
RX MEDLINE=98133310; PubMed=9475163;
RT "Human epsilon-sarcoglycan is highly related to alpha-sarcoglycan (dshalin), the limb girdle muscular dystrophy 2D gene.";
RL FEBS Lett. 422:27-32(1998).
RN [3]
RP SEQUENCE OF 269-413 FROM N.A.
RX MEDLINE=98070432; PubMed=9405466;
RA Ettlinger A.J., Feng G., Sanes J.R.;
RT "Epsilon-sarcoglycan, a broadly expressed homologue of the gene mutated in limb girdle muscular dystrophy 2D.";
RL J. Biol. Chem. 272:32534-32538(1997).
RN [4]
RP ERRATUM.
RA Ettlinger A.J., Feng G., Sanes J.R.;
RL J. Biol. Chem. 273:19922-19922(1998).
CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Sarcolemmal (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SCGE-1 (SHOWN HERE) AND SCGE-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: UBQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
CC -----
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CC -----
CC EMBL; AF031920; AAC14021.1; ALT_INIT.
CC EMBL; AF036364; AAC04368.1; -
CC EMBL; AJ000534; CAA04167.1; -
CC Genew: HGNC:10808; SCGE.
CC MIM: 604149; -
CC Cytoskeleton; Transmembrane; Glycoprotein; Signal;
KW Alternative splicing.

FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 438 EPSILON-SARCOGLYCAN.
FT DOMAIN 23 293 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 294 314 POTENTIAL.
FT DOMAIN 315 438 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 211 317 CYS-RICH.
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 395 419 MISSING (IN ISOFORM SCGE-2).
SQ SEQUENCE 438 AA; 49754 MW; D87D1899E9C16F23 CRC64;
OY 1 MTEQOWNFAGIEAA 14
1:111111:
DB 390 MOTOQWSPFAPVQAQ 403
Query Match 48.1%; Score 38; DB 1; Length 438;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 1 MTEQOWNFAGIEAA 14
1:111111:
DB 390 MOTOQWSPFAPVQAQ 403
RESULT 8
CADD_ECOLI STANDARD: PRT; 444 AA.
AC P23691;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable cadaverine/lysine antiporter.
GN CADD OR PA132 OR Z5735 OR ECSS114.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105022; PubMed=1370290;
RA Watson N., Dunyak D.S., Rosey E.L., Slonczewski J.L., Olson E.R.;
RT "Identification of elements involved in transcriptional regulation of the Escherichia coli cad operon by external pH.";
RL J. Bacteriol. 174:530-540(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210511; PubMed=1556085;
RA Meng S.-Y., Bennett G.N.;
RT "Nucleotide sequence of the Escherichia coli cad operon: a system for neutralization of low extracellular pH.";
RL J. Bacteriol. 174:2659-2669(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=9534362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.T., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDJ933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocitis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
 RA Kohara S., Shiba T., Hattori M., Shlnagawa H.,
 RT *Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.*;
 RL DNA Res. 8:11-22(2001).
 CC -1- FUNCTION: PROBABLE CADAVERINE/LYSINE ANTI-PORTER OR PART OF IT.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- INDUCTION: AT LOW PH IN THE PRESENCE OF LYSINE AND ACHELYVES
 CC MAXIMAL LEVEL UNDER ANAEROBIC CONDITIONS.
 CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
 CC PERMEASES.
 CC -----
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 CC -----
 DR EMBL: M67452; AAA23532.1; -;
 DR EMBL: M76411; AAA23535.1; -;
 DR EMBL: U14003; AAA97032.1; -;
 DR EMBL: AE000486; AAC77093.1; -;
 DR EMBL: AE005647; AAG59332.1; -;
 DR EMBL: AF002568; BAB38537.1; -;
 DR PIR: B41968; B41968.
 DR PIR: A41842; A41842.
 DR Ecogene: EG10132; CADB.
 DR Interpro: IPR002293; AA/tel_primease.
 DR Interpro: IPR004841; Permease.
 DR Pfam: PF00324; aa_permeases; 1.
 DR Trigram: TRIGR00905; 2A0302; 1.
 KW Transport; Antiport; Amino-acid transport; Transmembrane;
 KW Inner membrane; Complete proteome.
 FT TRANSMEM 7 27 POTENTIAL.
 FT TRANSMEM 35 55 POTENTIAL.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 95 115 POTENTIAL.
 FT TRANSMEM 123 143 POTENTIAL.
 FT TRANSMEM 149 169 POTENTIAL.
 FT TRANSMEM 193 213 POTENTIAL.
 FT TRANSMEM 222 242 POTENTIAL.
 FT TRANSMEM 250 270 POTENTIAL.
 FT TRANSMEM 273 293 POTENTIAL.
 FT TRANSMEM 323 343 POTENTIAL.
 FT TRANSMEM 354 374 POTENTIAL.
 FT TRANSMEM 384 404 POTENTIAL.
 FT TRANSMEM 405 425 POTENTIAL.
 SQ SEQUENCE 444 AA; 46665 MW; E87913B449B0500A CRC64;
 Query Match 48.1%; Score 38; DB 1; Length 444;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 6 WNFAGIEAAMA 15
 Db 198 MAEFGVESAA 207
 RESULT 9
 HMCM_PIG STANDARD; PRT; 508 AA.
 AC 002734;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor
 DE (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A
 DE synthase).
 GN HMGCS2.

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RX MEDLINE=97293201; PubMed=9164842;
 RA Adams S.H., Albo C.S., Asins G., Hegardt F.G., Marrero P.F.;
 RT *gene expression of mitochondrial 3-hydroxy-3-methylglutaryl-CoA
 RT synthase in a poorly ketogenic, mammal: effect of starvation during
 RT the neonatal period of the piglet.*;
 RL Biochem. J. 324:65-73(1997).
 CC -1- FUNCTION: THIS ENZYME CONDENSES ACETYL-CoA WITH ACETOACETYL-CoA
 CC TO FORM HMG-CoA, WHICH IS THE SUBSTRATE FOR HMG-CoA REDUCTASE.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxy-3-methylglutaryl-CoA + CoA -
 CC acetyl-CoA + H(2)O + acetoacetyl-CoA.
 CC -1- PATHWAY: RESPONSIBLE, TOGETHER WITH HMG-CoA LYASE FOR KETONE
 CC BODY BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE HMG-CoA SYNTHASE FAMILY.
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 CC -----
 DR EMBL: U90884; AAC48727.1; -;
 DR Interpro: IPR000590; HMG-CoA_synth.
 DR Pfam: PF01154; HMG-CoA_synth; 1.
 DR PROSITE: PS01226; HMG-CoA SYNTHASE; 1.
 KW lyase; Cholesterol biosynthesis; Mitochondrion; Transit peptide;
 KW Multigene family.
 FT TRANSMEM 1 37 MITOCHONDRION (PROBABLE).
 FT CHAIN 38 508 HYDROXYMETHYLGUTARYL-CoA SYNTHASE.
 FT ACT_SITE 166 166 POTENTIAL.
 SQ SEQUENCE 508 AA; 56933 MW; 5479DE6F70B3C0F6 CRC64;
 Query Match 48.1%; Score 38; DB 1; Length 508;
 Best Local Similarity 70.0%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 3 EOOMFAGIE 12
 Db 278 EKWMKQAGIE 287
 RESULT 10
 DREB_CHICK STANDARD; PRT; 652 AA.
 AC P18302; Q91358; Q91359;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Drebrin (Developmentally regulated brain protein).
 GN DBN1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS E1 AND E2).
 RX TISSUE=Brain;
 RX MEDLINE=89089137; PubMed=3208110;
 RA Kojima N., Kato Y., Shitao T., Obata K.;
 RT *Nucleotide sequences of two embryonic drebrins, developmentally
 RT regulated brain proteins, and developmental change in their mRNAs.*;
 RL Brain Res. 464:207-215(1988).
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORM A).
RA MEDLINE-93368392; PubMed-8361332;
RX Kojima N., Shirao T., Obara K.;
RT "Molecular cloning of a developmentally regulated brain protein,
RT chicken drebrin A and its expression by alternative splicing of the
RT drebrin gene.";
RL Brain Res. Mol. Brain Res. 19:101-114(1993).
CC -1- FUNCTION: DREBRIN MIGHT PLAY SOME ROLE IN CELL MIGRATION,
CC EXTENSION OF NEURONAL PROCESSES AND PLASTICITY OF DENDRITES,
CC RESPECTIVELY. BINDS F-ACTIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms: A (shown here), E1 and E2;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: BRAIN NEURONS.
CC -1- MISCELLANEOUS: DREBRIN ARE CLASSIFIED INTO TWO FORMS OF THE
CC EMBRYONIC TYPE (E1 AND E2) AND ONE FORM OF THE ADULT TYPE (A). THE
CC TIME COURSE OF THEIR APPEARANCE ARE DIFFERENT FROM EACH OTHER.
CC THEIR STRUCTURES ARE CLOSELY RELATED.
CC -----
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CC -----
DR EMBL: M36961; AAA8750.1; -
DR EMBL: S65296; AAB28012.1; -
DR EMBL: S65296; AAB28012.1; JOINED.
DR EMBL: S65280; AAB28012.1; JOINED.
DR EMBL: S65281; AAB28012.1; JOINED.
DR EMBL: S65288; AAB28012.1; JOINED.
DR EMBL: S65289; AAB28012.1; JOINED.
DR EMBL: S65290; AAB28012.1; JOINED.
DR EMBL: S65291; AAB28012.1; JOINED.
DR EMBL: S65292; AAB28012.1; JOINED.
DR EMBL: S65294; AAB28012.1; JOINED.
DR EMBL: S65267; AAB28011.2; -
DR EMBL: S65230; AAB28010.1; -
DR PIR: A43776; A43776.
DR InterPro: IPR002108; Actbind_cofln.
DR Pfam: PF00241; coflin_ADF.1.
DR SMART: SM00102; ADF.1.
KW Actin-binding; Neurone; Alternative splicing.
FT DOMAIN 47 50 POLY-GLY.
FT DOMAIN 332 339 POLY-SER.
FT DOMAIN 542 552 POLY-GLU.
FT DOMAIN 643 646 POLY-GLU.
FT VARSPLC 317 362 MISSING (IN ISOFORM E1).
FT VARSPLC 307 405 MISSING (IN ISOFORM E2).
FT CONFLICT 552 552 E -> EE (IN REF. 1).
SQ SEQUENCE 652 AA: 71535 MW: 8672CA549833E65 CRC64:
Query Match 48.1%; Score 38; DB 1; Length 652;
Best Local Similarity 57.1%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE-21316449; PubMed-11294830;
RA Tse W.T., Tang J., Jin O., Korsgren C., John K.M., Kung A.L.,
RA Gwynn B., Peters L.L., Lux S.E.;
RT "A new spectrin, beta-IV, has a major truncated isoform that
RT associates with promyelocytic leukemia protein nuclear bodies and the
RT nuclear matrix.";
RL J. Biol. Chem. 276:23974-23985(2001).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1 TO 4).
RX MEDLINE-20539976; PubMed-11086001;
RA Begins S., Aguilaro D., Dirks R., Jr., Maksimova E., Stabach P.,
RA Hetmel J.-M., Zhang J.-P., Philbrick W., Stepnev V., Ort T.,
RA Solimena M.;
RT "BetaIV spectrin, a new spectrin localized at axon initial segments
RT and nodes of ranvier in the central and peripheral nervous system.";
RL J. Cell Biol. 151:985-1002(2000).
RN [3]
RN SEQUENCE OF 386-2382 FROM N.A. (ISOFORM 1).
RP TISSUE=Brain;
RC MEDLINE-20450683; PubMed-1097877;
RX Nagase T., Kikuno R., Nakayama M., Hirotsawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms: 1 (shown here), 2, 3 and 4; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic
CC islets.
CC -1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.
CC -----
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CC -----
DR EMBL: AF311855; AAG42473.1; -
DR EMBL: AF082075; AAG38874.1; -
DR EMBL: AY004226; AAF93171.1; -
DR EMBL: AY004226; AAF93172.1; -
DR EMBL: AY004227; AAF93173.1; -
DR EMBL: AB046862; BAB13468.1; -
DR HSSP: Q01082; 1BKR.
DR GeneW: HGNC:14896; SPTBN4.
DR MIM: 606214; -
DR InterPro: IPR001589; Actbind_actnln.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR001849; PH.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR001605; Spectrin_PH.
DR Pfam: PF00169; PH.3.
DR Pfam: PF00307; CH.2.
DR Pfam: PF00435; Spectrin.56.
DR PRINTS: PR00683; SPECTRINPH.
DR SMART: SM00033; CH.2.
DR SMART: SM00233; PH.1.
DR SMART: SM00150; SPEC.16.
DR PROSITE: PS00019; ACTININ.1.
DR PROSITE: PS00020; ACTININ.2.
DR PROSITE: PS50021; CH.2.
DR PROSITE: PS50003; PH_DOMAIN.1.

KW Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
 KM Alternative splicing.
 FT DOMAIN 1 282 ACTIN-BINDING (BY SIMILARITY).
 FT DOMAIN 61 165 CH 2.
 FT DOMAIN 180 282 SPECTRIN 1.
 FT REPEAT 309 334 SPECTRIN 2.
 FT REPEAT 398 419 SPECTRIN 3.
 FT REPEAT 429 533 SPECTRIN 4.
 FT REPEAT 535 642 SPECTRIN 5.
 FT REPEAT 644 771 SPECTRIN 6.
 FT REPEAT 773 879 SPECTRIN 7.
 FT REPEAT 881 985 SPECTRIN 8.
 FT REPEAT 1019 1086 SPECTRIN 9.
 FT REPEAT 1088 1197 SPECTRIN 10.
 FT REPEAT 1199 1303 SPECTRIN 11.
 FT REPEAT 1305 1408 SPECTRIN 12.
 FT REPEAT 1410 1513 SPECTRIN 13.
 FT REPEAT 1515 1619 SPECTRIN 14.
 FT REPEAT 1621 1725 SPECTRIN 15.
 FT REPEAT 1727 1832 SPECTRIN 16.
 FT REPEAT 1834 1940 SPECTRIN 17.
 FT REPEAT 1942 2046 SPECTRIN 18.
 FT REPEAT 2048 2107 PH.
 FT DOMAIN 2418 2527 MISSING (IN ISOFORM 3).
 FT VARSPLIC 1 1257 AVQAGSLRQGNIGYQGEAVTRLLER -> MPYPSCS
 FT VARSPLIC 1258 1286 SAPSLGPIPPQIQGLEARRH (IN ISOFORM 3).
 FT VARSPLIC 1287 1309 NOENLRQAOOMOKHLDLELOH -> CLIHALLHPME
 FT VARSPLIC 1310 2564 PPLPRSS (IN ISOFORM 2).
 FT VARSPLIC 2113 2134 MISSING (IN ISOFORM 2).
 FT VARSPLIC 2155 2564 E -> PRREDLNPVGVDOPQHTKPSLPKPRANKETAR
 FT CONFLICT 604 608 RODTCL (IN ISOFORM 4).
 FT CONFLICT 714 714 MISSING (IN ISOFORM 4).
 FT CONFLICT 1189 1189 L -> S (IN REF. 2).
 FT CONFLICT 1193 1193 E -> K (IN REF. 2).
 FT CONFLICT 1331 1331 E -> K (IN REF. 2).
 FT CONFLICT 1331 1331 G -> S (IN REF. 1).
 SQ SEQUENCE 2564 AA: 288982 MW: 52CDE7D1D601ECC CRC64;

Query Match 48.1%; Score 38; DB 1; Length 2564;
 Best Local Similarity 60.0%; Pred. No. 2; 2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 QWNPAGIEAA 14
 DB 1021 QWRLSGLEAA 1030

RESULT 12
 MTO4_SYNY3
 ID MTO4_SYNY3 STANDARD; PRT: 211 AA.
 AC P73161;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical methyltransferase sl11300 (EC 2.1.1.-).
 GN SL11300.
 OS *Synechocystis* sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).
 CC -1- FUNCTION: PROBABLE METHYLTRANSFERASE.
 CC -1- SIMILARITY: BELONGS TO THE UPF0155 FAMILY.
 CC -----
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 CC -----
 DR EMBL: D90904; BAA17187.1; ALT_INIT.
 DR InterPro: IPR004395; Cons_hypoth91.
 DR InterPro: IPR003358; Methyltransf_4.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF02390; Methyltransf_4; 1.
 DR TrnFRAMS: TrnR00091; Cons_hypoth91, 1.
 KW Hypothetical protein; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 211 AA: 24416 MW: 71A13BD64B1FC898 CRC64;

Query Match 46.8%; Score 37; DB 1; Length 211;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 7; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTEQ--QWNPAGIE 12
 DB 52 MAQHPDWNFLGVE 65

RESULT 13
 COMT_RAT
 ID COMT_RAT STANDARD; PRT: 264 AA.
 AC P22734;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Catechol O-methyltransferase, membrane-bound form (EC 2.1.1.6)
 DE (MB-COMT) [contains: Catechol O-methyltransferase, soluble form
 DE (S-COMT)].
 GN COMT.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94107221; PubMed=8280056;
 RA Tenhunen J., Uimannen I.;
 RT "Production of rat soluble and membrane-bound catechol O-
 RT methyltransferase forms from bifunctional mRNAs.";
 RL Biochem. J. 296:595-600(1993).
 RN [2]
 RP SEQUENCE OF 11-264 FROM N.A.
 RX MEDLINE=91033034; PubMed=2227437;
 RA Salminen M., Lundstrom K., Tiiigmann C., Savolainen R., Kalkkainen N.,
 RA Uimannen I.;
 RT "Molecular cloning and characterization of rat liver catechol-O-
 RT methyltransferase.";
 RL Gene 93:241-247(1990).
 RN [3]
 RP SEQUENCE OF 11-472 FROM N.A., AND CHARACTERIZATION OF THE TWO FORMS.
 RX MEDLINE=92111472; PubMed=1765063;
 RA Uimannen I., Lundstrom K.;
 RT "Cell-free synthesis of rat and human catechol O-methyltransferase.
 RT Insertion of the membrane-bound form into microsomal membranes in
 RT vitro.";
 RL Eur. J. Biochem. 202:1013-1020(1991).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF SOLUBLE FORM.
 RX MEDLINE=94173341; PubMed=8127373;

RA Vldgren J., Svensson L.A., Liljas A.;
 RT "Crystal structure of catechol O-methyltransferase.";
 CC Nature 368:354-358(1994).
 CC -1- FUNCTION: CATALYZES THE O-METHYLATION, AND THEREBY THE
 CC INACTIVATION, OF CATECHOLAMINE NEUROTRANSMITTERS AND CATECHOL
 CC HORMONES. ALSO SHORTENS THE BIOLOGICAL HALF-LIVES OF CERTAIN
 CC NEUROACTIVE DRUGS, LIKE L-DOPA, ALPHA-METHYL DOPA AND
 CC ISOPROTERENOL.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + catechol = S-
 CC adenosyl-L-homocysteine + guaiacol.
 CC -1- COFACTOR: MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (isoform S-COMT). Type II
 CC membrane protein (isoform MB-COMT).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a membrane-bound form/MB-COMT
 CC (shown here) and a soluble form/S-COMT; are produced by
 CC alternative initiation.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: TO OTHER MAMMALIAN CATECHOL-O-METHYLTRANSFERASE.
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 CC -----
 DR EMBL: Z12651; CAI78276.1; -
 DR EMBL: M60754; AAA40882.1; ALT_INIT.
 DR EMBL: M60753; AAA40881.1; ALT_INIT.
 DR PIR: J00787; J00787.
 DR PIR: S22090; S22090.
 DR PDB: 1JUL-96.
 DR InterPro: IPR002935; Methyltransferf_3.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF01596; Methyltransferf_3; 1.
 DR Transferrase; Methyltransferase; Neurotransmitter degradation;
 KW Catecholamine metabolism; Transmembrane; Signal-anchor; Magnesium;
 KW Alternative initiation; 3D-structure.
 FT CHAIN 1 264 CATECHOL-O-METHYLTRANSFERASE, MEMBRANE-
 FT BOUND ISOFORM.
 FT CHAIN 45 264 CATECHOL-O-METHYLTRANSFERASE, SOLUBLE
 FT INIT_MET 44 44 ISOFORM.
 FT TRANSMEM 3 19 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT ACT_SITE 187 187
 FT ACT_SITE 242 242
 FT METAL 184 184 MAGNESIUM.
 FT METAL 212 212 MAGNESIUM.
 FT METAL 213 213 MAGNESIUM.
 SQ SEQUENCE 264 AA; 29597 MW; F535DF49C062854 CRC64;
 Query Match 46.8%; Score 37; DB 1; Length 264;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MTEOONPAGTE 12
 DB 141 ITDOMLNFAGLQ 152
 RESULT 14
 G3P_ESCBL STANDARD: PRT: 294 AA.
 AC P24749;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
 DE (Fragment).
 GN GAP.
 OS Escherichia blattae.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=563;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29907, ATCC 33429, and ATCC 33430;
 RX MEDLINE=92065252; PubMed=1955870;
 RA Lawrence J.G., Ochman H., Harl D.L.;
 RT "Molecular and evolutionary relationships among enteric bacteria.";
 CC J. Gen. Microbiol. 137:1911-1921(1991).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 CC DEHYDROGENASE FAMILY.
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 CC -----
 DR EMBL: M63358; AAA23837.1; -
 DR EMBL: M63359; AAA23852.1; -
 DR EMBL: M63360; AAA23855.1; -
 DR HSSP: P06977; 1GAD.
 DR InterPro: IPR00173; GAP_dhdrogenase.
 DR Pfam: PF00044; gpdh.C; 1.
 DR Pfam: PF02800; gpdh.C; 1.
 DR PROSITE: PS00721; GAPDH; 1.
 KW Glycolysis; Oxidoreductase; NAD.
 FT NON_TER 1 1
 FT BINDING 135 135 GLYCERALDEHYDE 3-PHOSPHATE.
 FT ACT_SITE 162 162 ACTIVATES THIOL GROUP DURING CATALYSIS.
 FT NON_TER 294 294
 SQ SEQUENCE 294 AA; 31372 MW; 18562CB398177D8B CRC64;
 Query Match 46.8%; Score 37; DB 1; Length 294;
 Best Local Similarity 54.5%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 5 OMNFGIRAA 15
 DB 69 KWNAGVEVA 79
 RESULT 15
 YD59_SCHPO STANDARD: PRT: 335 AA.
 ID YD59_SCHPO
 AC Q10312; Q9JUL8;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C6C3.09 in chromosome I.
 GN SPAC6C3.09.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Hucke E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandut R., Furnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerretti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Siparovsky G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -----
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CC -----
DR EMBL: Z69731; CAB40281.1; -
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 37948 MW; C1CD4E5850BAD323 CRC64;
OY 6 WNFAGIEA 13
DB 290 WNFAGIES 297

Query Match 46.8%; Score 37; DB 1; Length 335;
Best Local Similarity 62.5%; Pred. NO. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Search completed: July 3, 2003, 14:05:51
Job time : 7.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:03:50 ; Search time 12.5 Seconds
(without alignments)
115.361 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQOWNFAGIEAANA 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being predicted,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	95	2 A70803	early secretory an
2	45	57.0	476	2 S71360	noea protein - rhi
3	45	57.0	476	2 H85313	NOEA host specific
4	43	54.4	217	2 A82491	fine protein VCA01
5	43	54.4	247	2 H90825	hypothetical prote
6	42	53.2	369	2 E86554	Fe-S oxidoreductas
7	42	53.2	672	2 G72069	conserved hypotet
8	42	53.2	539	2 E87276	glucose-6-phosphat
9	42	53.2	723	2 E87706	prolyl oligopeptid
10	41	51.9	176	1 F64864	protein-disulfide
11	41	51.9	176	2 H90838	hypothetical prote
12	41	51.9	176	2 H85696	hypothetical prote
13	41	51.9	445	2 D82342	probable cadaverin
14	41	51.9	471	2 E69435	hypothetical prote
15	40	50.6	38	2 H82256	hypothetical prote
16	39	49.4	219	2 AG2036	hypothetical prote
17	39	49.4	328	2 A70145	prolipoprotein dia
18	39	49.4	393	2 AH2150	hypothetical prote
19	39	49.4	482	2 T01762	hypothetical prote
20	39	49.4	714	2 G86844	hypothetical prote
21	39	49.4	916	2 D83093	secretion protein
22	38.5	48.7	392	2 A87572	aminotransferase,
23	38	48.1	252	2 PC1140	cellulase (EC 3.2.
24	38	48.1	284	2 E82868	hypothetical prote
25	38	48.1	297	2 AD2851	cytochrome c1 floc
26	38	48.1	305	1 H75285	probable phosphos
27	38	48.1	319	2 B97628	cytochrome c1 (AFL
28	38	48.1	443	2 AE0826	probable cadaverin
29	38	48.1	444	2 A41842	lysine/cadaverine

30	38	48.1	444	2 B91268	transport protein
31	38	48.1	444	2 H86108	transport of lysin
32	38	48.1	593	2 I51213	trehalin - chick
33	38	48.1	607	2 A43776	trehalin B2 - chick
34	37	46.8	61	2 E86084	hypothetical prote
35	37	46.8	192	1 S75273	hypothetical prote
36	37	46.8	229	1 D90002	hypothetical prote
37	37	46.8	251	2 C81816	hypothetical prote
38	37	46.8	256	2 AD1115	hypothetical prote
39	37	46.8	257	2 AE1476	hypothetical prote
40	37	46.8	264	2 S22090	catechol O-methylt
41	37	46.8	267	2 A87404	ribosomal protein
42	37	46.8	294	2 I41220	glycerinaldehyde-3-p
43	37	46.8	326	2 A41862	C-5 lyase (OHR326)
44	37	46.8	335	2 T39033	hypothetical prote
45	37	46.8	348	2 A12475	hypothetical prote

ALIGNMENTS

```
RESULT 1
A70803
early secretory antigen target esat6 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: A70803 $49174
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MIMD:98295587; PMID:9634230
A:Accession: A70803
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-95 <COL>
A:Cross-references: 1-95 <COL>
A:Experimental source: strain H37RV
R:Soerensen, A.L.; Nagai, S.; Houen, G.; Andersen, P.; Andersen, A.B.
submitted to the EMBL Data Library, June 1994
A:Reference number: S49174
A:Accession: S49174
A:Molecule type: DNA
A:Residues: 1-13, 'R', 15-22, 'S', 24-95 <SOE>
A:Cross-references: EMBL:X79562; NID:9531708
C:Genetics:
A:Gene: esat6

Query Match          100.0%  Score 79;  DB 2;  Length 95;
Best Local Similarity 100.0%;  Pred. NO. 1.3e-06;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 MTEQOWNFAGIEAANA 15
DB 1 MTEQOWNFAGIEAANA 15

RESULT 2
S71360
noea protein - Rhizobium meliloti
C:Species: Rhizobium meliloti
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C:Accession: S71360; S71358
R:Ardourel, M.; Lortet, G.; Maillet, F.; Roche, P.; Truchet, G.; Prome, J.C.; Rosebn
submitted to the EMBL Data Library, May 1995
A:Reference number: S71360
A:Accession: S71360
A:Molecule type: DNA
A:Residues: 1-476 <ARD>
A:Cross-references: EMBL:U26430; NID:91326068; PIDN:MAC44091.1; PID:91326070
A:Experimental source: strain RCR2011
```

R.Ardourel, M.; Lorete, G.; Maillet, F.; Roche, P.; Truchet, G.; Prome, J.C.; Rosenberg, M.; Microbiol. 17, 687-699, 1995
A:Title: In Rhizobium meliloti, the operon associated with the nod box n5 comprises nodI
A:Reference number: S71357; MUID:96111489; PMID:8801423
A:Accession: S71358
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 304-339 <ARM>
A:Cross-references: EMBL:U26430
A:Experimental source: strain RCR2011 (-S047)
C:Genetics:
A:Gene: noeA
C:Superfamily: Rhizobium meliloti noeA protein
C:Keywords: nodulation

Query Match 57.0%; Score 45; DB 2; Length 476;
Best Local Similarity 63.6%; Pred. No. 5.7;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 5 OMNFAGIEAAA 15
:|||||:|
DB 100 EMSFAGLKAAA 110

RESULT 3
H95313
Noea host specific nodulation protein [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: H95313
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, J.; Katman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95313
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <NUR>
A:Cross-references: GB:AE006469; PIDN:AAK65074.1; PID:g14523508; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galbert, F.; Flann, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Hymn, R.W.; Jones, T.; Science 293, 666-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Katman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: noeA
A:Genome: plasmid
C:Superfamily: Rhizobium meliloti noeA protein

Query Match 57.0%; Score 45; DB 2; Length 476;
Best Local Similarity 63.6%; Pred. No. 5.7;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 5 OMNFAGIEAAA 15
:|||||:|
DB 100 EMSFAGLKAAA 110

RESULT 4
AB2491
fne protein VCA0178 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: AB2491
R:Heideberg, J.F.; Eelsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, H.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: AB2491
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <HEI>
A:Cross-references: GB:AE004358; GB:AE003853; NID:9657566; PIDN:AAF96091.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0178
A:Map position: 2

Query Match 54.4%; Score 43; DB 2; Length 217;
Best Local Similarity 75.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TEQWLFAGIEA 13
|||||
DB 170 TEQWLFAGIEA 181

RESULT 5
H90825
hypothetical protein ECS1576 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: H90825
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: H90825
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAK34999.1; PID:g13361040; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS1576

Query Match 54.4%; Score 43; DB 2; Length 247;
Best Local Similarity 53.8%; Pred. No. 6.3;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 EQQWFGAGIEAAA 15
:|||||:|
DB 22 EQQWFGAGIEAAA 34

RESULT 6
E86554
Fe-S oxidoreductase [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: E86554
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: AB6491; MUID:20330349; PMID:10871362
A:Accession: E86554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-369 <STO>
A:Cross-references: GB:BA000008; NID:96978883; PIDN:BAK98719.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CP10513
C:Superfamily: hypothetical protein AF0390

Query Match 53.2%; Score 42; DB 2; Length 369;

A:Gene: dsbb; roxB
A:Map position: 25.5 min
C:Function:
A:Description: reoxidizes dsba protein specifically
A:Note: reaction depends on the presence of oxygen
C:Superfamily: protein-disulfide oxidoreductase dsbb
C:Keywords: Oxidoreductase; redox-active disulfide; transmembrane protein
F:16-32/Domain: transmembrane #status predicted <TM1>
F:49-65/Domain: transmembrane #status predicted <TM2>
F:146-162/Domain: transmembrane #status predicted <TM3>
F:144/Disulfide bonds: redox-active #status predicted

Query Match 51.9%; Score 41; DB 1; Length 176;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 ECOMNFAGIE 12
Db 132 EROMDFLE 141

RESULT 11

H90838
protein-disulfide oxidoreductase ECS1680 [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 01-Mar-2002
C:Accession: H90838
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90838
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-116 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA035103.1; PID:g13361144; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECS1680
C:Superfamily: protein-disulfide oxidoreductase dsbb

Query Match 51.9%; Score 41; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 ECOMNFAGIE 12
Db 132 EROMDFLE 141

RESULT 12

H85696
hypothetical protein dsbb [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002
C:Accession: H85696
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 528-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11205551
A:Accession: H85696
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-116 <STO>
A:Cross-references: GB:AE005174; NID:g12514882; PIDN:AA656036.1; GSPDB:GN00145; UMG:215
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: dsbb
C:Superfamily: protein-disulfide oxidoreductase dsbb

Query Match 51.9%; Score 41; DB 2; Length 176;

Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 ECOMNFAGIE 12
Db 132 EROMDFLE 141

RESULT 13

D82342
probable cadaverine/lysine antiporter Cdb VC0280 [imported] - Vibrio cholerae (strai
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82342
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
I, R.R.; Mekalanos, J.D.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82342
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-445 <HEI>
A:Cross-references: GB:AE004116; GB:AE003852; NID:g9654687; PIDN:AAF93455.1; GSPDB:GN
C:Experimental source: serogroup O1, strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0280
A:Map position: 1
C:Superfamily: L-lysine transport protein

Query Match 51.9%; Score 41; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 6 WNFAGIEA 15
Db 199 WNFVGEA 208

RESULT 14

E69435
hypothetical protein AF1486 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
C:Accession: E69435
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kalne, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69435
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-471 <ALE>
A:Cross-references: GB:AE001000; GB:AE000782; NID:g2689323; PIDN:AA89769.1; PID:g264
C:Superfamily: Methanobacterium conserved hypothetical protein MTH943

Query Match 51.9%; Score 41; DB 2; Length 471;
Best Local Similarity 61.5%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 ECOMNFAGIEA 15
Db 45 ECOMDFEKEADA 57

RESULT 15

H82256
hypothetical protein VC0978 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: H82256
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82256
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-38 <HEI>
A:Cross-references: GB:AE004179; GB:AE003852; NID:99655432; PIDN:AAF94140.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0978
A:Map position: 1

Query Match 50.6%; Score 40; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 MTEOQWNPAGIEAA 14
|||:|:
Db 18 MTINQWNIWGVA 31

Search completed: July 3, 2003, 14:07:18
Job time : 14.5 secs

ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-667-2

Query Match 48.1%; Score 38; DB 1; Length 410;
Best Local Similarity 41.7%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 ECOMNFAGIEA 14
:||||| : :
DB 50 KORNFGSVRSA 61

RESULT 11
US-08-579-667-6
Sequence 6, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: No. 5705624th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-667-6

Query Match 48.1%; Score 38; DB 1; Length 410;
Best Local Similarity 41.7%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 ECOMNFAGIEA 14

DB :||||| : :
50 KORNFGSVRSA 61

RESULT 12
US-08-579-667-8
Sequence 8, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: No. 5705624th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-667-8

Query Match 48.1%; Score 38; DB 1; Length 410;
Best Local Similarity 41.7%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 ECOMNFAGIEA 14
:||||| : :
DB 50 KORNFGSVRSA 61

RESULT 13
US-09-368-590-2
Sequence 2, Application US/09368590
Patent No. 6187563
GENERAL INFORMATION:
APPLICANT: Solimena, Michele
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-667-4

Query Match 53.2%; Score 42; DB 1; Length 413;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 ECOMNFAGIEA 14
DB 50 ECOMNFAGSVKSA 61

RESULT 8
US-08-685-808-3
Sequence 3, Application US/08685808
Patent No. 6048715

GENERAL INFORMATION:
APPLICANT: HAYNES, CHARLES A., et al
TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,808
FILING DATE: 24-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/505,860
FILING DATE: 24-JULY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CBDT.017.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-685-808-3

Query Match 48.1%; Score 38; DB 3; Length 155;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 OCOMNFAGIEA 13
DB 91 OCOMNFLEIQA 100

RESULT 9
US-08-505-860C-3
Sequence 3, Application US/08505860C
Patent No. 6174700
GENERAL INFORMATION:
APPLICANT: HAYNES, CHARLES A., et al

TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,860C
FILING DATE: 24-JULY-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CBDT.017.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-505-860C-3

Query Match 48.1%; Score 38; DB 4; Length 155;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 OCOMNFAGIEA 13
DB 91 OCOMNFLEIQA 100

RESULT 10
US-08-579-667-2
Sequence 2, Application US/08579667
Patent No. 5705624

GENERAL INFORMATION:
APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: NO. 5705624th Carolina
COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-99

Query Match 100.0%; Score 79; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEOQMFAGIEAAA 15
|||||
DB 1 MTEOQMFAGIEAAA 15

RESULT 5
US-08-465-640-2
Sequence 2, Application US/08465640
Patent No. 5955077
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: ANDERSEN, Ase Bengaard
APPLICANT: HASLOV, Kaare
APPLICANT: SORENSEN, Anne Lund
TITLE OF INVENTION: TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,640
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,182
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK94/00273
FILING DATE: 01-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSEN-3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-640-2

Query Match 100.0%; Score 79; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEOQMFAGIEAAA 15
|||||

DB 1 MTEOQMFAGIEAAA 15

RESULT 6
US-09-001-984C-77
Sequence 77, Application US/09001984C
Patent No. 6245331
GENERAL INFORMATION:
APPLICANT: Laal, Sumar
APPLICANT: Zolla-Pazner, Susan
APPLICANT: Bellisle, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-011
CURRENT APPLICATION NUMBER: US/09/001,984C
CURRENT FILING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: 60/034,003
PRIOR FILING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 77
LENGTH: 10
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-77

Query Match 65.8%; Score 52; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0024;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEOQMFAGI 11
|||||
DB 1 TEOQMFAGI 10

RESULT 7
US-08-579-667-4
Sequence 4, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: NO. 5705624th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3175
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 amino acids

OY 1 MTEOQWNFAGIEAAA 15
|||||
DB 1 MTEOQWNFAGIEAAA 15

RESULT 2

US-08-818-111-99
Sequence 99, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-99

Query Match 100.0%; Score 79; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNFAGIEAAA 15
|||||
DB 1 MTEOQWNFAGIEAAA 15

RESULT 3

US-09-056-556-104
Sequence 104, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-104

Query Match 100.0%; Score 79; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTEOQWNFAGIEAAA 15
|||||
DB 1 MTEOQWNFAGIEAAA 15

RESULT 4
US-09-072-596-99
Sequence 99, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twedlik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:

US-09-072-596-99
Sequence 99, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twedlik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 3, 2003, 14:04:30 ; Search time 11 Seconds
(without alignments)
40.122 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTEQOWNFAGIEAAA 15

Scoring table: BLOSUM62

Searched: GAPDP 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 10%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	51	4	US-08-818-112-104
2	79	100.0	51	4	US-08-818-111-99
3	79	100.0	51	4	US-09-056-556-104
4	79	100.0	51	4	US-09-072-596-99
5	79	100.0	95	4	US-08-465-640-2
6	52	65.8	10	4	US-09-001-984C-77
7	42	53.2	413	1	US-08-579-667-4
8	38	48.1	135	3	US-08-685-808-3
9	38	48.1	155	4	US-08-505-860C-3
10	38	48.1	410	1	US-08-579-667-2
11	38	48.1	410	1	US-08-579-667-6
12	38	48.1	410	1	US-08-579-667-8
13	38	48.1	2293	4	US-09-368-590-2
14	36	46.2	934	1	US-08-215-805A-80
15	36	45.6	602	4	US-09-149-727-2
16	36	45.6	607	4	US-09-149-727-8
17	36	45.6	608	4	US-08-637-670-36
18	36	45.6	618	4	US-09-149-727-4
19	36	45.6	3111	2	US-08-460-309-4
20	36	45.6	3111	2	US-08-125-077-4
21	35.5	44.9	593	1	US-08-202-389-12
22	35.5	44.9	593	1	US-08-018-129-5
23	35.5	44.9	593	2	US-08-448-250-5
24	35	44.3	360	4	US-09-509-902A-9
25	35	44.3	600	6	5268463-2
26	35	44.3	602	2	US-08-882-704A-5
27	35	44.3	602	4	US-09-151-957-5

28	35	44.3	602	6	5432081-2	Patent No. 5432081
29	35	44.3	603	3	US-09-149-727-6	Sequence 6, Appl1
30	35	44.3	832	4	US-08-630-820-7	Sequence 7, Appl1
31	35	44.3	1056	2	US-08-627-873-7	Sequence 7, Appl1
32	35	44.3	1242	2	US-09-488-270A-2	Sequence 2, Appl1
33	34.5	43.7	561	1	US-08-052-404-22	Sequence 22, Appl1
34	34.5	43.7	561	1	US-08-479-156-22	Sequence 37, Appl1
35	34	43.0	67	1	US-08-167-035-37	Sequence 37, Appl1
36	34	43.0	67	1	US-08-208-887A-37	Sequence 37, Appl1
37	34	43.0	67	2	US-08-539-005-37	Sequence 37, Appl1
38	34	43.0	67	4	US-09-280-598-57	Sequence 57, Appl1
39	34	43.0	201	3	US-08-816-346-6	Sequence 6, Appl1
40	34	43.0	201	4	US-09-335-411-6	Sequence 51, Appl1
41	34	43.0	409	1	US-08-190-802A-51	Sequence 3, Appl1
42	34	43.0	409	2	US-08-283-917-3	Sequence 3, Appl1
43	34	43.0	409	2	US-08-961-716-3	Sequence 3, Appl1
44	34	43.0	409	4	US-08-477-346-51	Sequence 51, Appl1
45	34	43.0	409	4	US-08-473-089-51	Sequence 51, Appl1

ALIGNMENTS

RESULT 1
US-08-818-112-104

; Sequence 104, Application US/08818112

; Patent No. 6290969

; GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skelky, Yasir A.W.

APPLICANT: Dillon, Davin C.

APPLICANT: Campos-Neto, Antonio

APPLICANT: Houghton, Raymond

APPLICANT: Vedvick, Thomas S.

APPLICANT: Twaizick, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818.112

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 104:

SEQUENCE CHARACTERISTICS:

LENGTH: 51 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-818-112-104

Query Match 100.0%; Score 79; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2,7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0;